

**REMARKS/ARGUMENTS**

Claim 20, which was previously dependent from claim 15, has been re-written to be dependent from claim 15 once again. The scope of claim 20 is intended to be returned to that of original claim 20 with the limitations from claim 15, which were presented for business considerations and to better tailor the claims to encompass commercially contemplated embodiments of the invention at the present time rather than in acquiescence to any rejection asserted by the U.S. Patent and Trademark Office (PTO). Support is provided at least by claim 20 as originally filed and claim 15.

Claims 42 and 43 have been canceled without prejudice for pursuit in a continuing application.

No new matter has been introduced, and entry of the amendments is respectfully requested.

**Telephonic Interview of 2 March 2005**

Applicants thank Examiners Zeman and SPE A. Marschal for the courtesy of a telephonic interview on 2 March 2005 with them and Nicole Verona, Esq., of the assignee of interest in the instant application, and the undersigned as participants. The interview began with a discussion of the asserted anticipation rejection based upon the patent to Hung (U.S. Patent 6,642,009). The undersigned pointed out that of all the “markers” disclosed by Hung, no combination of five or more of them that would overlap with the genes disclosed in the instant application. Examiner Zeman indicated that she would review this argument in a written response more closely in combination with the arguments, in the response filed 8 September 2004, traversing this same rejection.

The undersigned also pointed out Applicants’ understanding that the assertion of Hung under 35 U.S.C. § 102(e) based on the disclosure therein (as opposed to the claims) inherently includes the assertion that Hung placed his disclosed subject matter in the possession of the skilled artisan. This is in the absence of any disclosure of the nucleic acid sequence of any of the Hung “markers”. Thus Hung is being relied upon as providing possession of his disclosed

subject matter to the skilled artisan via a written description that does not include specific sequences.<sup>1</sup> This is in contrast to the instant application where the absence of nucleic acid sequence disclosure has been asserted as resulting in a failure “to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.” The undersigned pointed out that the requirements of the same standard of “possession” appeared to be different between what is required of the Hung reference and what is required of the instant application.

The interview then turned to the asserted rejection under 35 U.S.C. § 112, first paragraph. The undersigned presented information from the IMAGE Consortium website explaining how each “clone ID” was a unique reference identifier that identified a particular nucleic acid molecule clone. There was also an explanation of how these unique “clone ID” identifiers were included in various publicly accessible sequence databases, such as GenBank and dBest. The undersigned then presented Applicants’ view that an adequate written description of the claimed invention was already present in the instant application because all the disclosed genes, as well as the particular nucleic acid molecule clones and associated sequences, were *already known in the art* (as evidenced by the clone ID reference numbers used and the availability of sequence information from publicly accessible sources). The undersigned also pointed out that this assertion of an adequate written description is consistent with the inherent assertion (explained above) that the Hung specification placed the Hung disclosed subject matter into the possession of the skilled person.

The Examiners maintained the position that inclusion of sequence information for each disclosed gene or clone ID was necessary for an adequate written description. They further indicated that amendments to the instant specification to include sequences for each disclosed gene/clone ID as known at the time of the invention would not introduce new matter. SPE Marschal also indicated that inclusion of any updated or corrected sequence for each disclosed gene/clone ID would also not introduce new matter.

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<sup>1</sup> Of course this discussion of an adequate disclosure of Hung’s subject matter in the Hung reference does not alter Applicants’ view that the Hung reference does not affect the patentability of the instant application’s pending claims.

The undersigned stated that Applicants would consider the possibility of amending the specification to include sequence information. However, the undersigned also expressed Applicants' view that the Examiners' requirement for inclusion of known sequence information for each gene/clone ID (as described above) would simply be an exercise of including information that was known in the art at the time of the invention. Because it is axiomatic that knowledge known in the art does not have to be included for an adequate written description, the undersigned questioned the Examiners' position that inclusion of the sequence information (which is just knowledge known in the art) is needed for an adequate written description. The Examiners only responded by indicating that sequence information would provide information regarding sequences that could be used in the invention.

Claim Rejection under 35 USC § 112, first paragraph

Claims 15-21, 30-41 and 44-48 were rejected under 35 USC § 112, first paragraph as allegedly "failing to comply with the written description requirement." Specifically, the statement of the instant rejection alleges that the claims contain "subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention."

Applicants have carefully considered the results of the interview as summarized above and reviewed the statement of the instant rejection. Applicants will consider the option of revising the application to include sequence information as described above, and Applicants expressly reserve the right to do so.

Before addressing the statement of this rejection, Applicants respectfully wish to provide further information regarding the public knowledge and availability of the genes disclosed in the instant application. Specifically, the IMAGE Consortium discloses how clones of the disclosed genes are available from the American Type Culture Collection, Manassas, VA (ATCC). This is shown in attached Appendix 1, which has a screenshot of a page from the IMAGE Consortium website (at <http://image.llnl.gov/image/html/idistributors.shtml>), specifically pointing out multiple available sources for the clones. This is confirmed by the

ATCC website home page, where the top and bottom of the page are shown via two screenshots in Appendix 1. The second screenshot include a section entitled “Clone searching” which states

Finding the clone you need is easier than ever. Our new clone search allows you to search specifically by GenBank accession number, I.M.A.G.E. clone ID, or ATCC number. Look for a single clone or submit your entire list. We also offer a full range of clone plates and plate sets.  
[at <http://www.atcc.org/Home.cfm>]

The last screenshot in Appendix 1 is of the top of the clone search page at the ATCC website, which allows for searches based on IMAGE Consortium cloneID numbers. Based on the above, Applicants respectfully submit that no issue of public availability of the clones is present. The clones can readily be ordered and obtained and then used. The sequence inherent to each clone can be determined as desired. Accordingly, Applicants believe that an adequate written description is present without the need for sequence information in the instant application.

Applicants now turn to the statement of the instant rejection and their traversal thereof because they believe no *prima facie* case of an inadequate written description has been presented.

As noted above in the description of the interview, Applicants do not understand why the inclusion of sequence information known in the field (and publicly available) at the time of the invention is requested for an adequate written description.

The statement of the rejection asserts that “[a]rguing both the written description and art rejections together is inappropriate, as each rejection is assessed on its own merit.” Applicants respectfully disagree with the above at least in situations like the instant application, where the inconsistent standards for *possession* by the skilled person as applied in the prior art rejection and *possession* by the skilled person as applied in the written description rejection are inconsistent. Applicants respectfully submit that it is inappropriate and arbitrary to apply one level of the *possession* test in the prior art rejection and another level in the instant rejection.

The statement of the rejection asserts that the instant “specification does not provide enough information for one of skill in the art to be able to obtain the proper sequences of the allegedly identified genes in order to make the arrays required.” Applicants respectfully disagree because contrary to the assertion, the skilled person can obtain sequence information about the genes identified in the instant application by use of the cloneID reference and/or the description of the gene. Information is available on both the IMAGE Consortium website as well as sequence database websites like GenBank as described above, where sequence information is indexed by cloneID identifiers. Additionally, the actual clones of each cloneID are publicly accessible as explained by the IMAGE Consortium, which even addresses the issue of clones that are no longer available because of the redundancy with other clones, which would of course be the replacement for an unavailable clone based on the redundancy.

Additionally, Applicants point out that the skilled person only needs to identify *the expression of* the genes disclosed in the instant application. As such, a partial sequence, as well as a sequence with enough complementarity to serve as a specific probe for the expression of the disclosed genes, is sufficient to be used in the practice of the claimed invention, such as by use of a probe containing array. There is simply no requirement to use the whole of the disclosed genes to detect their expression. Indeed, the instant application includes the recognition that it is not the particular sequences of the genes that is relevant but the identification of the expression of the genes as being correlated with stages of breast cancer. In the alternative, of course, an entire clone of one, or more, of the disclosed genes can be used to detect its, or their, expression.

The statement of the rejection also asserts that the “CloneID numbers are referencing a non-stable website which does not provide adequate written description of the reference sequences.” Applicants respectfully disagree because it is not clear as to what issue is raised by the alleged “non-stable” nature of the website. There is no indication that the cloneID identifiers are unstable with respect to specific clones. Moreover, the possibility that the sequence information associated with each cloneID identifier may be “non-stable” is irrelevant, because the nature of the actual clone remains constant. Applicants respectfully submit that the written description requirement in the instant application should be focused on the actual subject

of the genes (and detecting the expression thereof) rather than on merely a view of the genes. Stated differently, the written description requirement should be focused on the actual gene or genes, the expression of which is/are detected, rather than on the perception of what sequence to detect. This is emphasized by the fact that the invention can be practiced with use of the disclosed genes (via the disclosed clones) to be detected without actually knowing the particular sequence of the clone used.

The statement of the rejection further asserts that the disclosed sequences are not related in sequence or function and so “there is no structural or functional basis for identifying what sequences could be used in the invention.” While the Examiner may be correct in that many of the disclosed genes are unrelated in terms of their sequence, Applicants respectfully point out that the instant invention is based in part on the discovery of a common functionality of the disclosed genes in the ability to determine breast cancer progression based on the expression of the genes. This is a definite and clear function that is common to the disclosed genes, which are a defined set based upon the specific tables in the instant application.

Applicants are not aware of any requirement in U.S. patent law for a disclosure of “why” or “how” the expression of the disclosed genes are correlated with breast cancer progression. Accordingly, any requirement for disclosure of a “structure-function” relationship or “mechanism” by which the disclosed genes function is misplaced.

In light of the above, Applicants respectfully submit that the instant rejection is misplaced and may be properly withdrawn.

Claim Rejections under 35 USC § 102

Claims 15-21, 30-41 and 44-48 were rejected under 35 USC § 102(e) as allegedly anticipated by Hung (USP 6,642,009). Applicants point out that claim 20 has been revised as presented above.

Based in part on the interview as described above, Applicants have prepared a summary of the “markers” disclosed by Hung. The following table provides an alphabetical listing of the “markers” disclosed by Hung along with the number (from column 6, line 58, to column 9, line 37) and/or location of the disclosure in the Hung document.

<b>Hung “marker” name/description</b>	<b>Numerical identifier from columns 6-9 of Hung or other Hung location identifier</b>
absorption of a marker (like iodide) [this is not disclosed as based on the expression of any gene]	31
apoptosis-related protein	18
Bcl-2 gene product	16
breast cancer associated gene (BRCA)	30
BU101 protein	10
CD66a	12
CDw60 protein	36
cell adhesion molecule 5.2 (CAM 5.2)	14
carcino embryonic antigen (CEA)	col. 1, line 44
complement regulatory protein CD 46	22
complement regulatory protein CD 59	23
c-raf kinase	11
E2F1	4
Fibroblast growth factor	32
G-actin	col. 4, line 61
Insulin-like growth factor-1 (IGF-1 protein)	34
KAI1/CD82	28
Kallikrein 6 (zyme/protease M/neurosin or polypeptide hK6)	39
KL-1	13
leptin	15
Lg	3

lipocalin NGAL	19
FRA3B site (loss of heterozygosity there at) [this is not disclosed as based on the expression of any gene]	26
loss of heterozygosity [this is not disclosed as based on the expression of any gene]	25
lysophosphatidic acid (LPA) or a receptor thereof	1
MAGUK/ZO-1	6
Mammary expressed enzymes (cytochrome P450s, catechol-O-methyltransferase, epoxide hydrolase, peroxidases, glutathione-S-transferases, N-acetyltransferases, and sulfotransferases)	37
Mammastatin protein or polypeptide	38
Maspin protein	35
MRP-1/CD9	27
nuclear matrix 23 (nm23)	17
FHIT gene	24
p53 gene	col. 4, line 61
palladin	2
prothymosin alpha (PTA)	8
Repressor of estrogen receptor activity (REA)	7
T1A12/mac 25	5
thymosin beta-15	20
TMS-1	29
TNF-related apoptosis-inducing ligand (TRAIL)	9
tumor amplified kinase STK15 (BTAK or aurora2)	21
Vascular endothelial growth factor (VEGF)	33

Tables 2-5 of the instant application have been revised to be in alphabetical order based on the Description of each gene disclosed therein. Copies of these alphabetically reordered Tables are attached to the end of this response as Attachment A.<sup>2</sup> A comparison of the above table to the alphabetically reordered Tables in the Appendix is facilitated by the ability to look alphabetically for the same name.

Applicants have performed previously this type of comparison and noted the results in the response filed 8 September 2004. Specifically, there are only four possible “markers” from Hung that are in common with the instant application. These are the nuclear matrix 23 (nm23) marker (in column 7, lines 63-67 of Hung and possibly in instant Table 2); the complement regulatory protein CD 59 marker (in column 8, lines 22-25 of Hung and possibly in instant Table 3); the catechol-O-methyltransferase marker (in column 9, line 20 of Hung and possibly in instant Tables 2, 4, and 5); and the kallikrein 6 marker (column 9, lines 31-37 of Hung and possibly in instant Tables 2, 3, and 4).

Thus even assuming *in arguendo*, and with the reservation that Hung possibly does not actually disclose the use of the genes of Tables 2, 3, 4 and 5 (disclosed in part via the cloneID identifiers), that the above Hung markers are those disclosed in the respectively identified Tables, there is still no disclosure of the use of five or more genes of any one of the Tables as required by the instant claims.

Therefore, Applicants respectfully submit that this rejection may be properly withdrawn.

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<sup>2</sup> The alphabetically reordered Tables have the same content as the corresponding Tables in the instant application with the following exception: cloneIDs that were not listed with a Description have been updated to include the Description available at the IMAGE Consortium website on March 4, 2005. These Descriptions do not change the inherent nature of the clone identified by the cloneID identifier. The Descriptions are in bold text in the alphabetically reordered Tables of the Appendix.

The Descriptions included by the update is solely for the purpose to facilitate the comparison of the information in the Tables to the Hung disclosure and is not intended to introduce new matter into the instant application.

Appl. No. 10/028,018  
Am dt. dated 5 March 2005  
Reply to Office Action of 6 January 2005

PATENT

**CONCLUSION**

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 858-350-6100.

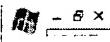
Respectfully submitted,



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KL:ps  
60436260 v1

## Appendix 1



### The I.M.A.G.E. Consortium

*"Sharing resources to achieve a common goal - the discovery of all genes"*

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#### I.M.A.G.E. Consortium Distributors

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I.M.A.G.E. clones and associated products may be obtained from any of our authorized distributors. On-line ordering through the WWW (or by email) is encouraged. To aid us in tracking I.M.A.G.E. resource use, distributors periodically inform the I.M.A.G.E. Consortium of the number of clones sent to each user; however the specific clones (i.e. CloneIDs) ordered are considered a confidential matter between each distributor and their customers.

Within the United States, the distributors are:

- [American Type Culture Collection](#), Manassas, VA
- [Open Biosystems](#), Huntsville, AL
- [Research Genetics/Invitrogen](#), Carlsbad, CA

In Europe, I.M.A.G.E. distributors are:

- [MRC geneservice](#), Babraham, UK
- [RZPD German Resource Center for Genome Research](#), Berlin Germany

For a complete listing of associated contact information, [click here](#).

A Good Faith Agreement governs the usage of I.M.A.G.E. clones and associated products. The wording of the original document was revised in 9/00; the current agreement is now available and covers all I.M.A.G.E. clones and products retroactive to the beginning of the project.

I.M.A.G.E. downloads and parses GenBank records to find entries regarding I.M.A.G.E. clones. Groups sequencing I.M.A.G.E. clones can help us with this task by trying to conform to a few standards with respect to the format they use when submitting sequences. A [Genbank Suggested Format](#) document gives further details.

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The genome of *Silicibacter pomeroyi* shows unique adaptations to its marine environment (*Nature* 432: 910-913, 2004). We have the culture and the DNA from this organism, the first member of a major heterotrophic clade to be sequenced. (Photo courtesy of James R. Heniksen, University of Georgia, and Frank Mayer, Universität Göttingen.)

**The means to an end**

We've illustrated the intrinsic and extrinsic [apoptosis pathways](#) to show the genes associated with each step. You can follow links to NCBI gene data and learn about clone availability in ATCC's catalog. Apoptosis detection kits and related cell lines are also noted when appropriate.

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products for stem cell research, more individually characterized nonhuman embryonic stem (ES) cells and lineage- or tissue-specific neonatally derived stem cells from several species. In addition, we offer ES-qualified support products like feeder layer cells, media, sera, and reagents.

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## Appendix 2

The Tables provided below are alphabetically reordered versions, based on the Description of each gene disclosed therein, of Tables 2-5 of patent application 10/028,018. The Tables have no change in content with the following exception: cloneIDs that were not listed with a Description have been updated to include the Description available at the IMAGE Consortium website on March 4, 2005. These entries are in bold text in the alphabetically reordered Tables.

The inclusion of Descriptions for these cloneIDs is solely for the purpose to facilitate the comparison of the information in the Tables to the Hung disclosure and does not introduce new matter into the application.

**Table 2** (in alphabetical order)

CloneID	Weight	Description
770785	0.6613519	1,2-alpha-mannosidase IC
1574058	1.0651351	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
430614	0.476288	2,3-bisphosphoglycerate mutase
838366	0.702617	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)
713782	0.7484589	a disintegrin and metalloproteinase domain 15 (metarginidin)
704254	0.6653635	a disintegrin and metalloproteinase domain 8
1738208	0.7565056	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4
488505	0.808712	accessory proteins BAP31/BAP29
1587863	0.4270229	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3- oxoacyl-Coenzyme A thiolase)
823930	0.5633774	actin related protein 2/3 complex, subunit 1A (41 kD)
1473922	0.7892502	actin related protein 2/3 complex, subunit 3 (21 kD)
340558	0.7791736	actin related protein 2/3 complex, subunit 5 (16 kD)
2549634	0.5572052	activator of S phase kinase
210862	0.4692392	acyl-Coenzyme A oxidase 1, palmitoyl
343607	0.5029133	AD-015 protein
323693	0.5975785	adaptor-related protein complex 1, sigma 1 subunit
788641	0.4703576	adaptor-related protein complex 1, sigma 2 subunit
739109	0.5874334	adaptor-related protein complex 2, sigma 1 subunit

796757 0.5585876 adaptor-related protein complex 3, sigma 1 subunit  
279970 0.7040135 adenosine A2a receptor  
327635 0.5368033 adenylate kinase 1  
51532 0.6504769 ADP-ribosylation factor-like 6 interacting protein  
712139 -1.4736508 ADP-ribosylation factor-like 7  
46248 0.7510436 ADP-ribosyltransferase (NAD<sup>+</sup>; poly (ADP-ribose) polymerase)  
774446 0.4567242 adrenomedullin  
2095066 -0.9972552 alcohol dehydrogenase 1C (class I), gamma polypeptide  
814798 -1.2748689 aldehyde dehydrogenase 1 family, member A3  
47853 0.4231314 aldehyde dehydrogenase 4 family, member A1  
812105 0.4424976 ALL1-fused gene from chromosome 1q  
1635320 -1.2878152 amiloride-sensitive cation channel 2, neuronal  
2250839 0.4994848 androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)  
505289 0.5080495 angiotensin II, type I receptor-associated protein  
208718 -1.1498532 annexin A1  
666879 -1.3624072 annexin A8  
239568 0.661735 annexin A9  
1435862 0.9500093 antigen identified by monoclonal antibodies 12E7, F21 and O13  
1568825 0.5205165 Arg/Abl-interacting protein ArgBP2  
767487 0.4729158 ariadne (Drosophila) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1  
2110511 0.8471736 artemin  
377275 -1.2665702 ataxia-telangiectasia group D-associated protein  
782439 0.454474 ATP synthase, H<sup>+</sup> transporting, mitochondrial F0 complex, subunit e  
815737 -1.1116223 ATP synthase, H<sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle  
825386 0.5487104 ATP synthase, H<sup>+</sup> transporting, mitochondrial F1F0, subunit d  
2018821 0.6205344 ATPase inhibitor precursor  
754625 0.4236648 ATPase, Class II, type 9A  
266312 0.4201146 ATPase, Cu<sup>++</sup> transporting, beta polypeptide (Wilson disease)

810725 0.8510425 ATPase, H<sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD  
813256 -1.0407652 ATP-binding cassette, sub-family B (MDR/TAP), member 1  
767798 0.6192232 ATX1 (antioxidant protein 1, yeast) homolog 1  
753897 0.5153412 autocrine motility factor receptor  
244764 0.5424555 B7 homolog 3  
796694 0.7317383 baculoviral IAP repeat-containing 5 (survivin)  
1709791 1.0378948 BAI1-associated protein 1  
1609665 -0.9851713 BarH-like homeobox 2  
1456701 0.7934389 B-cell CLL/lymphoma 9  
1565079 0.4415966 B-cell linker  
2244196 0.6807351 B-cell receptor-associated protein BAP29  
814899 0.5142481 BCL2/adenovirus E1B 19kD-interacting protein 3-like  
2043167 0.7224903 BCL2-associated athanogene 3  
1916575 0.4923447 BCL2-interacting killer (apoptosis-inducing)  
1568561 0.4808662 BCL2-like 1  
809357 0.7535411 Bernardinelli-Seip congenital lipodystrophy 2 (seipin)  
786069 -1.1143906 beta-site APP-cleaving enzyme  
741977 0.7715372 B-factor, properdin  
1420370 0.6531171 biliverdin reductase B (flavin reductase (NADPH))  
empty-31 0.4726918 blank  
1733262 0.6293971 BLu protein  
811024 0.7117211 bone marrow stromal cell antigen 2  
1616253 0.5190257 breast carcinoma amplified sequence 1  
191904 0.6141265 BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog  
781047 0.4699376 budding uninhibited by benzimidazoles 1 (yeast homolog)  
271472 0.7901735 C3HC4-like zinc finger protein  
754653 0.4707927 cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (*Drosophila*) homolog  
841679 0.6762195 calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)  
49630 0.6027878 calcium channel, voltage-dependent, L type, alpha 1D subunit  
346134 0.5132068 calcium-regulated heat-stable protein (24kD)  
772913 -1.0122192 calreticulin  
785793 0.5072717 capping protein (actin filament) muscle Z-line, alpha 1

649084	0.5099122	carbonic anhydrase XI
67765	0.6967324	carboxypeptidase M
509823	0.6334191	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
744417	0.8409538	carnitine acetyltransferase
30170	0.4936252	caspase 3, apoptosis-related cysteine protease
72778	-1.3873177	caspase 7, apoptosis-related cysteine protease
1878409	-1.1144369	catechol-O-methyltransferase
51083	0.6544472	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)
345538	0.4550133	cathepsin L
842994	0.7563101	cathepsin Z
377461	-1.4787671	caveolin 1, caveolae protein, 22kD
1572298	-0.9906095	CD3Z antigen, zeta polypeptide (TiT3 complex)
725454	0.7335223	CDC28 protein kinase 2
786067	0.5361882	cell division cycle 25B
415102	0.5465851	cell division cycle 25C
376516	0.5906248	cell division cycle 4-like
2017415	0.5353408	centromere protein A (17kD)
366067	0.6416356	cerebellar degeneration-related protein (62kD)
1626996	-1.0328113	c-fos induced growth factor (vascular endothelial growth factor D)
2108077	0.7700354	CGI-112 protein
726439	0.5080059	CGI-143 protein
1947647	0.5064941	CGI-147 protein
753400	0.496254	CGI-204 protein
811774	1.0617336	CGI-49 protein
624667	0.7524325	CGI-92 protein
884425	0.5265114	chaperonin containing TCP1, subunit 5 (epsilon)
882484	0.6521026	chaperonin containing TCP1, subunit 7 (eta)
283023	-1.0825166	chemokine (C-X3-C) receptor 1
72050	0.5722845	chloride channel, nucleotide-sensitive, 1A
293569	0.5162069	chromosome 1 open reading frame 21
1492426	0.9397097	chromosome 19 open reading frame 3
824052	0.8650616	chromosome 6 open reading frame 1
469383	0.4607375	chromosome 8 open reading frame 1
731308	0.8166873	citrate synthase
124331	0.624455	cleavage and polyadenylation specific factor 5, 25 kD subunit

510794	0.4691467	c-myc binding protein
1656062	0.593408	coagulation factor XII (Hageman factor)
1632252	0.474559	complement component 1, q subcomponent, alpha polypeptide
2322079	0.4309341	<b>contig C019549, human</b>
127646	0.5838788	<b>contig C030249, human</b>
823909	0.4215098	<b>contig C039966, human</b>
770992	0.4346858	<b>contig C056172, human</b>
897770	0.4836347	<b>contig C071196, human</b>
108425	0.6761526	<b>contig C076797, human</b>
283751	0.4179154	cortistatin
489823	0.5666593	COX17 (yeast) homolog, cytochrome c oxidase assembly protein
1416782	0.5657017	creatine kinase, brain
839736	-1.4745405	crystallin, alpha B
1555924	-1.1342985	CSR1 protein
701751	0.6824676	cut ( <i>Drosophila</i> )-like 1 (CCAAT displacement protein)
487444	0.4887966	cyclic AMP phosphoprotein, 19 kD
742595	0.8291965	cyclin-dependent kinase 5
700792	0.5493223	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
1323448	1.5470535	cysteine-rich protein 1 (intestinal)
360254	-1.0325653	cysteine-rich, angiogenic inducer, 61
196189	0.6338517	cytochrome b-5
1455394	0.4455695	cytochrome c
278531	0.6737637	cytochrome c oxidase subunit VIc
1601947	0.5744444	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
884511	0.4199518	cytochrome c oxidase subunit VIIb
38356	0.4173012	cytochrome P450, subfamily 46 (cholesterol 24-hydroxylase)
768064	0.7743382	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1
724888	0.4196322	cytochrome P450, subfamily IVB, polypeptide 1
810039	0.4491986	defender against cell death 1
296702	0.5162041	deiodinase, iodothyronine, type I
1492468	0.647846	DEME-6 protein
810156	0.6266313	deoxythymidylate kinase (thymidylate kinase)
1161564	-1.5917197	desmuslin
842980	0.7284256	developmentally regulated GTP-binding protein 1
795401	0.5264278	diacylglycerol O-acyltransferase (mouse) homolog

813387 0.5460577 diaphorase (NADH/NADPH) (cytochrome b-5 reductase)  
760299 -1.8654555 dickkopf (*Xenopus laevis*) homolog 3  
742685 -1.4440371 disabled (*Drosophila*) homolog 2 (mitogen-responsive phosphoprotein)  
767761 0.6142782 DKFZP434B168 protein  
825740 0.5931142 DKFZp434J1813 protein  
366353 0.7664569 DKFZP564C186 protein  
770766 0.6193342 DKFZP564C1940 protein  
345423 0.4538841 DKFZP564M112 protein  
294397 0.5066683 DKFZP586A0522 protein  
2011515 0.6774452 DKFZP586B0923 protein  
202514 0.6872212 DNA (cytosine-5-)methyltransferase 3 alpha  
809466 0.5532437 DNA segment on chromosome 19 (unique) 1177 expressed sequence  
754046 0.4550413 DNA segment on chromosome X (unique) 9879 expressed sequence  
263727 0.5313082 DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)  
454896 0.4760701 DnaJ (Hsp40) homolog, subfamily A, member 2  
1637302 0.424164 DNAJ domain-containing  
2018527 0.599584 dolichyl-phosphate mannosyltransferase polypeptide 3  
884462 -1.2078038 Down syndrome critical region gene 1  
154610 0.4948571 dynactin 4  
782688 0.4694868 dynein, axonemal, light intermediate polypeptide  
593023 -1.0135883 dystrobrevin, beta  
1864302 -1.0099902 E74-like factor 5 (ets domain transcription factor)  
781017 -1.3232108 early growth response 2 (Krox-20 (*Drosophila*) homolog)  
188335 -1.0161259 egf-like module containing, mucin-like, hormone receptor-like sequence 2  
295986 0.5544422 emopamil-binding protein (sterol isomerase)  
2248488 0.6337488 ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate)  
1687976 0.4257058 endoplasmic reticulum chaperone SIL1, homolog of yeast  
74070 0.4390933 endosulfine alpha  
823574 0.5978052 endosulfine alpha  
122147 0.4652151 engulfment and cell motility 2 (ced-12 homolog, *C. elegans*) (ELMO2), *Homo sapiens*  
366834 0.5191005 envoplakin

153760	-1.1793765	EphB1
811088	-1.1625002	ephrin-B3
1577736	-1.035115	epidermal growth factor (beta-urogastrone)
109863	0.8066906	epithelial membrane protein 2
34093	-1.2156885	EST
594500	0.7935958	EST
1641894	0.5587185	EST
358267	0.6962436	EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
34150	-1.0302576	ESTs
40027	-1.0057005	ESTs
41826	0.4264531	ESTs
70606	0.4475592	ESTs
83358	0.4397161	ESTs
139660	-1.0134677	ESTs
140635	0.4384907	ESTs
162308	-1.023071	<b>ESTs</b>
162308	-1.2006293	ESTs
196435	-1.2282733	ESTs
214996	0.45033	ESTs
250313	0.5649247	ESTs
266500	0.5135558	ESTs
281190	-0.9830533	ESTs
290101	0.4800598	ESTs
344091	0.6381862	ESTs
365738	0.7709456	ESTs
415816	-0.9954308	ESTs
564847	0.757516	ESTs
564981	0.6712134	ESTs
754628	0.7573763	ESTs
757191	-1.2902603	ESTs
784105	0.6003082	ESTs
814209	0.5736866	ESTs
827171	0.7211896	ESTs
855707	0.4456433	ESTs
1027283	0.4628012	ESTs
1257131	-1.1566479	ESTs
1500162	0.7571399	ESTs
1517749	0.5665848	ESTs
1536006	0.7499887	ESTs
1537001	0.4539586	ESTs
1557637	0.4705061	ESTs
1558233	0.5101529	ESTs
1585492	0.4571478	ESTs
1700436	0.6215741	ESTs

1899312 0.4418248 ESTs  
2046679 0.4579596 ESTs  
431505 0.6534315 ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]  
289760 -1.5534789 ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]  
  
79726 0.5078677 ESTs, Highly similar to T46395 hypothetical protein DKFZp434I1120.1 [H.sapiens]  
  
279720 0.5645072 ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]  
725978 0.7010756 ESTs, Moderately similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]  
  
530197 0.6659784 ESTs, Moderately similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]  
  
593431 0.6578268 ESTs, Moderately similar to CEGT\_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]  
  
345670 -1.889471 ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]  
  
529843 -1.2405917 ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]  
  
120749 0.6172281 ESTs, Moderately similar to KIAA1215 protein [H.sapiens]  
  
179212 0.4594831 ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]  
  
160192 -1.4695435 ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]  
2017721 0.4268089 ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]  
810497 0.4572069 ESTs, Weakly similar to A35363 synapsin I splice form a [H.sapiens]  
73009 0.516678 ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]  
726699 0.6131491 ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]  
  
746163 0.4863317 ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

2016908 0.9615102 ESTs, Weakly similar to CA13\_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]  
488642 0.5560728 ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]  
128695 0.4340119 ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]  
1640821 0.8544081 ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]  
841621 0.4466003 ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]  
742707 0.7955239 ESTs, Weakly similar to MUC2\_HUMAN MUCIN 2 PRECURSOR [H.sapiens]  
2029173 0.9672743 ESTs, Weakly similar to N-WASP [H.sapiens]  
1583198 0.4350835 ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]  
2572170 0.5852444 ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]  
358936 0.6441198 ESTs, Weakly similar to T2D3\_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]  
743589 0.7372744 ESTs, Weakly similar to T2D3\_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]  
35147 1.3764654 ESTs, Weakly similar to unnamed protein product [H.sapiens]  
488202 0.9501137 ESTs, Weakly similar to YZ28\_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]  
796542 -1.5553964 ets variant gene 5 (ets-related molecule)  
811837 -1.1269309 eukaryotic translation elongation factor 1 alpha 1  
811837 -1.1468554 eukaryotic translation elongation factor 1 alpha 1  
469151 0.4622121 eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD )  
74566 0.4279059 exportin 1.(CRM1, yeast, homolog)  
301122 0.6299499 extracellular matrix protein 1  
782503 0.4205398 fatty acid desaturase 1  
1758590 0.6074571 fatty-acid-Coenzyme A ligase, long-chain 3  
1469148 0.467634 FGFR1 oncogene partner

809464 0.426456 fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)

752631 0.7139862 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)

789012 0.6794432 fibulin 2

813616 0.5574238 FK506-binding protein like

376875 0.6286902 flavin containing monooxygenase 1

131839 -1.7087069 folate receptor 1 (adult)

772220 0.4475721 for protein disulfide isomerase-related

628955 -0.997687 forkhead box O1A (rhabdomyosarcoma)

796475 -1.0217348 four and a half LIM domains 3

52419 -1.2004086 Friedreich ataxia region gene X123

2309073 0.5617024 frizzled (Drosophila) homolog 5

298122 -1.5678888 frizzled (Drosophila) homolog 7

1499828 0.5479012 fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)

183200 0.5801312 fumarylacetoacetate hydrolase (fumarylacetoacetate)

2016775 -1.0761731 G protein-coupled receptor, family C, group 5, member B

842825 0.7235007 G1 to S phase transition 1

1854539 0.4824023 GAP-associated tyrosine phosphoprotein p62 (Sam68)

214068 0.4383007 GATA-binding protein 3

1393018 0.701717 general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD )

741474 0.8925439 glucose phosphate isomerase

2018337 0.6828744 glucosidase, beta; acid (includes glucosylceramidase)

1609836 1.2349106 glutamate-ammonia ligase (glutamine synthase)

731044 0.8657953 glutaredoxin 2

1848977 0.5519913 glycerol kinase

344720 -1.7951928 glycophorin C (Gerbich blood group)

358217 0.4507923 glypcan 4

686552 0.7506994 golgi phosphoprotein 1

1556433 -1.4191955 GRO3 oncogene

752643 0.5774681 group XII secreted phospholipase A2

85195 0.4207753 growth arrest and DNA-damage-inducible, gamma

796181 -1.1584587 growth arrest-specific 6

788654 0.8886269 **growth factor receptor-bound protein 2**

788654 1.4818381 growth factor receptor-bound protein 2

810063	0.8168926	growth factor, erv1 ( <i>S. cerevisiae</i> )-like (augmenter of liver regeneration)
51741	0.5795151	GTP-binding protein
308466	0.8803492	GTP-binding protein Sara
40773	0.4510289	guanine nucleotide binding protein (G protein), alpha z polypeptide
292213	0.5883092	guanine nucleotide binding protein (G protein), beta polypeptide 2
66317	0.5648355	H1 histone family, member 2
283919	1.118257	H2A histone family, member L
488964	1.1545223	H2A histone family, member O
290841	0.9562201	H2B histone family, member A
1500000	1.3204029	H2B histone family, member B
430235	0.585372	H2B histone family, member Q
815781	0.5340254	heat shock 105kD
471568	1.1466811	hematological and neurological expressed 1
1569187	-1.9090486	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
345833	0.4187433	heterogeneous nuclear ribonucleoprotein A/B
770845	0.6253839	hexokinase 1
1637282	0.542121	hexokinase 2
345787	0.4734963	highly expressed in cancer, rich in leucine heptad repeats
172517	0.6701228	hippocalcin-like 1
1434948	0.4771454	HIV TAT specific factor 1
1434905	0.4382073	homeo box B7
347726	0.4837701	homeo box D8
1592715	0.6637095	Homer, neuronal immediate early gene, 3
742581	0.433453	<i>Homo sapiens</i> cDNA FLJ10366 fis, clone NT2RM2001420
1474424	0.6006702	<i>Homo sapiens</i> cDNA FLJ12758 fis, clone NT2RP2001328
212542	0.6938079	<i>Homo sapiens</i> cDNA FLJ12900 fis, clone NT2RP2004321
270826	-1.0112851	<i>Homo sapiens</i> cDNA FLJ13329 fis, clone OVARC1001795
283739	0.5276555	<i>Homo sapiens</i> cDNA FLJ14028 fis, clone HEMBA1003838
366156	0.4563893	<i>Homo sapiens</i> cDNA FLJ14028 fis, clone HEMBA1003838
825327	0.7622414	<i>Homo sapiens</i> cDNA FLJ14105 fis, clone MAMMA1001202
35626	0.4509825	<i>Homo sapiens</i> cDNA FLJ14201 fis, clone NT2RP3002955

1492780 0.5555908 Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409  
770675 0.4319407 Homo sapiens cDNA: FLJ21323 fis, clone COL02374  
131094 0.9518372 Homo sapiens cDNA: FLJ21587 fis, clone COL06946  
814528 0.9569471 Homo sapiens cDNA: FLJ22139 fis, clone HEP20959  
753071 -1.8417236 Homo sapiens cDNA: FLJ22528 fis, clone HRC12825  
840266 -1.6530726 Homo sapiens cDNA: FLJ22667 fis, clone HSI08385  
745394 0.4374406 Homo sapiens cDNA: FLJ23249 fis, clone COL04196  
727078 0.7472345 Homo sapiens cDNA: FLJ23602 fis, clone LNG15735  
823694 0.5321203 Homo sapiens chromosome 19, BAC CIT-HSPC\_204F22  
(BC228680), complete sequence; contains bacterial  
insertion element  
649977 0.5002695 Homo sapiens clone CDABP0014 mRNA sequence  
796723 1.0724133 Homo sapiens clone CDABP0014 mRNA sequence  
488404 -1.1981268 Homo sapiens clone TUA8 Cri-du-chat region mRNA  
768452 0.5237494 Homo sapiens EST from clone 491476, full insert  
743977 0.5237158 Homo sapiens mRNA for TL132  
327506 0.5092192 Homo sapiens mRNA full length insert cDNA clone  
EUROIMAGE 327506  
70245 -1.0348655 Homo sapiens mRNA full length insert cDNA clone  
EUROIMAGE 50374  
44292 0.8732235 Homo sapiens mRNA; cDNA DKFZp434C107 (from clone  
DKFZp434C107)  
1871116 -1.0975491 Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone  
DKFZp434C1714); partial cds  
1883028 0.5828007 Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone  
DKFZp434J1912)  
2016648 0.8263671 Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone  
DKFZp434N1728)  
265103 0.6548137 Homo sapiens mRNA; cDNA DKFZp547M123 (from clone  
DKFZp547M123)

565319 1.2369212 Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)

813265 -1.2549431 Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)

486683 -1.6799604 Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)

1844765 0.5670398 Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)

1461477 0.509331 Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)

1584540 -1.0077508 Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)

132857 -1.0989746 Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)

22917 -1.5156635 Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)

74738 0.5835427 Homo sapiens, clone IMAGE:3535294, mRNA, partial cds

1631735 0.7505843 Homo sapiens, clone IMAGE:3604336, mRNA, partial cds

186768 0.7298378 Homo sapiens, clone IMAGE:3604869, mRNA

292770 0.8570995 Homo sapiens, clone IMAGE:3627860, mRNA, partial cds

1652310 0.4512689 Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds

810002 -1.7256692 Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds

810567 0.4702908 Homo sapiens, clone MGC:3182 IMAGE:3356293, mRNA, complete cds

121436 0.4691298 Homo sapiens, clone MGC:4677 IMAGE:3532809, mRNA, complete cds

1635665 0.5714089 Homo sapiens, RIKEN cDNA 2010100O12 gene, clone MGC:14813 IMAGE:4133274, mRNA, complete cds

491527 0.5116183 Homo sapiens, Similar to CG7083 gene product, clone MGC:10534 IMAGE:3957147, mRNA, complete cds

130835 0.4946783 Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA

41123 0.481642 Homo sapiens, Similar to RIKEN cDNA 2210021G21 gene, clone MGC:14859 IMAGE:3621871, mRNA, complete cds

839746 0.5031787 Homo sapiens, Similar to RIKEN cDNA 5830420C20 gene, clone IMAGE:3633379, mRNA, partial cds

1492238 1.1991653 HSPC003 protein

1600239 0.421459 HSPC037 protein

796469 1.1850928 HSPC150 protein similar to ubiquitin-conjugating enzyme

772925 0.5940171 HSPCO34 protein

470099 0.7343404 HT002 protein; hypertension-related calcium-regulated gene

241043 0.5545302 Human clone 137308 mRNA, partial cds

813675 0.4614894 Human D9 splice variant B mRNA, complete cds

178805 1.22225746 Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG

811585 0.7087617 huntingtin (Huntington disease)

1554549 1.1440029 hydroxyacyl glutathione hydrolase

813419 0.8043966 hydroxyacyl-Coenzyme A dehydrogenase, type II

256619 0.7395032 hydroxysteroid (17-beta) dehydrogenase 7

80764 0.6765616 hypothetical protein

139354 0.5318709 hypothetical protein

140289 0.6205892 hypothetical protein

595213 0.5775511 hypothetical protein

785766 0.6058332 hypothetical protein

810402 0.7407907 hypothetical protein

811848 -1.3549757 hypothetical protein

825822 0.5097808 hypothetical protein

841260 0.5285587 hypothetical protein

299815 0.5485843 hypothetical protein DC42

150118 0.4383146 hypothetical protein DKFZp434F054

32489 -1.0196444 hypothetical protein DKFZp566A1524

489351 0.65846 hypothetical protein DKFZp566J2046

746190 0.4291743 hypothetical protein DKFZp761B1514

76182 -1.2102812 hypothetical protein DKFZp761F241

66406 0.5706229 hypothetical protein DKFZp762E1312

51657 0.5736969 hypothetical protein ET

491465 0.5150527 hypothetical protein FLJ10035

767289 0.4432685 hypothetical protein FLJ10055

292936	0.4593712	hypothetical protein FLJ10468
753299	0.8679015	hypothetical protein FLJ10504
823907	0.4218216	hypothetical protein FLJ10511
504308	0.6041122	hypothetical protein FLJ10540
503889	0.7454098	hypothetical protein FLJ10656
40042	0.4604322	hypothetical protein FLJ10747
233349	0.762952	hypothetical protein FLJ10761
809512	0.4442565	hypothetical protein FLJ10767
246800	0.5625675	hypothetical protein FLJ10803
2052113	0.8307595	hypothetical protein FLJ10903
325515	0.4689353	hypothetical protein FLJ10980
126851	0.6559601	hypothetical protein FLJ11160
768570	0.8371438	hypothetical protein FLJ11280
266218	0.4934791	hypothetical protein FLJ11350
589232	0.7583348	hypothetical protein FLJ11506
489594	0.5308806	hypothetical protein FLJ11565
744994	0.4916322	hypothetical protein FLJ12242
743220	0.5242028	hypothetical protein FLJ12517
41569	0.7412357	hypothetical protein FLJ12650
731080	0.4979864	hypothetical protein FLJ12661
785795	0.660789	hypothetical protein FLJ12910
150003	0.77183	hypothetical protein FLJ13187
1605426	0.8909868	hypothetical protein FLJ13352
248649	0.761865	hypothetical protein FLJ13910
1554167	-1.4126653	hypothetical protein FLJ14529
1581941	0.5537015	hypothetical protein FLJ14540
259950	0.4187278	hypothetical protein FLJ14991
76196	0.4278385	hypothetical protein FLJ20062
1505038	1.2292506	hypothetical protein FLJ20171
489444	0.4741367	hypothetical protein FLJ20211
428582	0.4642013	hypothetical protein FLJ20296
2027952	0.437854	hypothetical protein FLJ20297
809507	0.4189998	hypothetical protein FLJ20568
502774	0.8091404	hypothetical protein FLJ20623
1636092	0.8997881	hypothetical protein FLJ20657
300632	-1.6969092	hypothetical protein FLJ21044 similar to Rbig1
1572710	0.4750848	hypothetical protein FLJ21213
85804	0.44449	hypothetical protein FLJ21918
429799	0.6012713	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
811907	0.5246416	hypothetical protein FLJ22056
510575	0.6040713	hypothetical protein FLJ22087
810939	0.4634658	hypothetical protein FLJ22169
2015517	0.6259564	hypothetical protein FLJ22237
1493218	-1.164886	hypothetical protein FLJ22297

1947381	0.5524634	hypothetical protein FLJ22329
37554	0.6574292	hypothetical protein FLJ22353
753378	0.6218232	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
757328	0.6097389	hypothetical protein FLJ22678
52103	0.432756	hypothetical protein FLJ23045
455275	0.4788778	hypothetical protein FLJ23469
144880	0.6332999	hypothetical protein from EUROIMAGE 1759349
1696757	0.6591801	hypothetical protein KIAA1165
625693	0.6744622	hypothetical protein MGC10911
781342	0.6159353	hypothetical protein MGC11115
1642496	0.4645092	hypothetical protein MGC11266
824879	0.8366695	hypothetical protein MGC11275
325606	0.7008219	hypothetical protein MGC14353
1898619	0.5880791	hypothetical protein MGC15737
68636	0.9562688	hypothetical protein MGC2477
490023	-1.3516302	hypothetical protein MGC2648
815501	0.4879053	hypothetical protein MGC2721
1869201	0.8202299	hypothetical protein MGC2745
1558642	0.4424721	hypothetical protein MGC2771
51773	0.7858986	hypothetical protein MGC3077
37708	0.8194577	hypothetical protein MGC3101
814443	-1.1905978	hypothetical protein MGC3232
42408	0.7559848	hypothetical protein MGC4604
123614	0.7117834	hypothetical protein MGC4675
120271	0.5626611	hypothetical protein MGC4692
120271	0.7208543	hypothetical protein MGC4692
812238	1.2132886	hypothetical protein MGC4692
1858892	0.9897362	hypothetical protein MGC4825
121251	0.6209436	hypothetical protein MGC5576
293727	0.5153298	hypothetical protein MGC861
810609	0.5036493	hypothetical protein PP1226
745606	1.3470375	hypothetical protein PP591
2028949	0.6662774	hypothetical protein PRO1855
625399	-1.0523138	hypothetical protein similar to beta-transducin family
743860	0.4189656	hypothetical protein, clone 2746033
897806	0.6470379	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
39884	0.9091807	IMP (inosine monophosphate) dehydrogenase 1
221295	0.6477514	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
788234	-1.4824055	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein

2051697	0.4197703	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
505243	-0.980381	inositol 1,4,5-triphosphate receptor, type 2
77533	0.435582	inositol polyphosphate-5-phosphatase, 40kD
207288	0.632639	insulin induced gene 1
814350	0.7701748	insulin-degrading enzyme
130201	-1.2885369	intercellular adhesion molecule 2
755599	0.6330221	interferon induced transmembrane protein 1 (9-27)
1592837	0.4355927	interferon induced transmembrane protein 2 (1-8D)
1159963	0.5133656	interferon regulatory factor 7
782513	0.5625811	interferon, alpha-inducible protein (clone IFI-6-16)
856447	0.4816395	interferon, gamma-inducible protein 30
1422723	0.4411931	interferon-induced protein 35
84295	0.4349213	interleukin 1 receptor antagonist
811920	-1.6924158	interleukin 11 receptor, alpha
1517171	0.7036866	interleukin 2 receptor, alpha
80344	-1.0323882	interleukin 7 receptor
859228	0.4942316	isocitrate dehydrogenase 1 (NADP+), soluble
869375	0.4958886	isocitrate dehydrogenase 2 (NADP+), mitochondrial
868128	0.8873517	JM4 protein
414992	0.587733	K562 cell-derived leucine-zipper-like protein 1
809784	-1.030253	kallikrein 6 (neurosin, zyme)
2243051	-0.9835274	kallikrein 8 (neuropsin/ovasin)
824962	0.595868	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
625234	0.62188	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
1474900	-1.1347123	keratin 15
1486533	0.441804	keratin 16 (focal non-epidermolytic palmoplantar keratoderma)
773922	0.7767604	KIAA0005 gene product
686172	0.7131363	KIAA0008 gene product
814054	0.958989	KIAA0040 gene product
898032	0.7852733	KIAA0097 gene product
530310	0.5686743	KIAA0143 protein
1517595	0.4409591	KIAA0175 gene product
43977	0.4309655	KIAA0182 protein
1473471	-1.2409979	KIAA0194 protein
49117	0.5274035	KIAA0215 gene product

782428	0.9524489	KIAA0250 gene product
1884404	0.6864546	KIAA0285 gene product
809944	0.7021108	KIAA0310 gene product
795805	0.5064099	KIAA0332 protein
773426	0.5941568	KIAA0391 gene product
221499	0.5317861	KIAA0508 protein
753162	-1.0416438	KIAA0603 gene product
725841	0.6051304	KIAA0662 gene product
1636166	-0.9969091	KIAA0668 protein
786265	0.5443881	KIAA0750 gene product
40173	0.7124913	KIAA0807 protein
366039	0.4701924	KIAA0892 protein
1679942	0.4215618	KIAA1053 protein
124447	0.679866	KIAA1184 protein
1640282	0.4205899	KIAA1240 protein
1518402	0.7150061	KIAA1361 protein
843054	0.5776102	KIAA1533 protein
149539	0.4671676	KIAA1700
277571	-1.2030738	KIAA1706 protein
753038	-1.1629978	kinesin family member C3
769942	0.509086	kinesin-like 4
343731	0.5365018	<b>Kruppel-like factor 2 (lung) (KLF2), Homo sapiens</b>
280249	0.6503028	Kruppel-like factor 7 (ubiquitous)
770355	0.6099761	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
767202	-1.3217103	latent transforming growth factor beta binding protein 2
897731	-0.9927981	latrophilin
199403	1.082569	lectin, galactoside-binding, soluble, 8 (galectin 8)
60565	0.720547	lethal giant larvae ( <i>Drosophila</i> ) homolog 2
470092	0.5429717	like-glycosyltransferase
2056139	-1.2697411	LIM domain protein
1469377	-1.6473741	lipoma HMGIC fusion partner-like 2
810947	0.5151346	LIS1-interacting protein NUDE1, rat homolog
825296	0.5178447	low density lipoprotein receptor defect C complementing
490778	0.6788304	low molecular mass ubiquinone-binding protein (9.5kD)
150314	0.6584621	lysophospholipase I
826363	0.6087183	lysophospholipase II
1631747	0.5245873	male-enhanced antigen
366100	-1.0467604	matrilin 2
470393	-1.2354879	matrix metalloproteinase 7 (matrilysin, uterine)
142586	0.602037	MCT-1 protein

2069602	0.4786416	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
200814	-1.7140538	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
729975	0.9149894	meningioma expressed antigen 5 (hyaluronidase)
1518890	0.7206844	metallothionein-like 5, testis-specific (tesmin)
878406	0.6750777	metaxin 1
2014034	0.8354357	methylene tetrahydrofolate dehydrogenase (NAD <sup>+</sup> dependent), methenyltetrahydrofolate cyclohydrolase
124298	0.6294358	microsomal glutathione S-transferase 3
564492	0.7672548	mitochondrial carrier homolog 2
359723	0.4630712	mitochondrial elongation factor G
491524	0.5175752	mitochondrial ribosomal protein L13
2019223	0.849044	mitochondrial ribosomal protein L17
788334	0.6427785	mitochondrial ribosomal protein L23
416436	0.4252319	mitochondrial ribosomal protein L24
417801	0.5414761	mitochondrial ribosomal protein L27
782608	0.8507815	mitochondrial ribosomal protein L9
1909574	0.4342055	mitochondrial ribosomal protein S11
590774	0.8100386	mitogen-activated protein kinase 13
2326057	0.61263	MLN51 protein
1075635	0.4495618	MLSN1- and TRP-related
450301	0.4380657	mutL ( <i>E. coli</i> ) homolog 3
611443	0.6244565	myoglobin
1473274	-1.1557062	myosin regulatory light chain 2, smooth muscle isoform
629944	0.4242364	myosin VB
744944	0.5482368	myosin VI
841308	-1.200964	myosin, light polypeptide kinase
840865	0.644011	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)
1456348	0.7397574	N-acetylneuraminic acid phosphate synthase; sialic acid synthase
66599	0.4639123	N-acetyltransferase 1 (arylamine N-acetyltransferase)
1635681	0.7152705	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)
951216	0.5291832	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)
487733-2	0.5844776	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)
487733	0.6745496	<b>NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)</b>

753457 0.4435792 NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD)  
(NADH-coenzyme Q reductase)

611467 0.4428543 NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD)  
(NADH-coenzyme Q reductase)

358609 0.5266332 NADH dehydrogenase (ubiquinone) flavoprotein 3 (10kD)

1762111 0.5272967 natriuretic peptide receptor C/guanylate cyclase C  
(atrionatriuretic peptide receptor C)

76605 0.9028609 nesca protein

838478 -1.5059801 neurocalcin delta

289428 -1.1923798 neurotrophic tyrosine kinase, receptor, type 2

877621 -1.3987023 nGAP-like protein

199645 0.6654138 nicastrin

811761 0.6587469 Nijmegen breakage syndrome 1 (nibrin)

825659 0.4515758 N-myc downstream regulated

75859 -2.4150177 N-myc downstream-regulated gene 2

845363 0.617901 non-metastatic cells 1, protein (NM23A) expressed in

726658 0.5157542 non-metastatic cells 3, protein expressed in

203003 0.6724027 non-metastatic cells 4, protein expressed in

795256 0.6974866 NPD007 protein

207794 0.4297389 nuclear factor (erythroid-derived 2), 45kD

416959 -1.051868 nuclear factor I/B

725649 0.4559473 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4

503851 0.564048 nuclear receptor co-repressor/HDAC3 complex subunit

773188 0.6270494 nuclear receptor subfamily 1, group D, member 2

1565455 0.4634802 nuclear receptor subfamily 2, group C, member 2

377384 0.4746085 nuclear receptor subfamily 2, group F, member 2

843070 -1.1647509 nucleoporin 88kD

769890 0.4647115 nucleoside phosphorylase

773674 0.6095732 oncogene TC21

1523225 0.4511104 oncostatin M receptor

66535 0.6088919 ornithine decarboxylase antizyme 2

782608 0.7230962 **ornithine decarboxylase antizyme 3 (OAZ3), Homo sapiens**

1753497 0.5485231 ovo (Drosophila) homolog-like 1

756442 0.7115925 P450 (cytochrome) oxidoreductase

781019 0.6819736 paraoxonase 2

81203	0.4391758	paraoxonase 3
785368	0.4411742	PDZ-binding kinase; T-cell originated protein kinase
1882697	-1.3873266	peanut ( <i>Drosophila</i> )-like 2
416676	-1.2751042	pellino ( <i>Drosophila</i> ) homolog 1
285377	-1.6514168	pellino ( <i>Drosophila</i> ) homolog 2
1587710	-1.0092611	period ( <i>Drosophila</i> ) homolog 1
1573251	0.823025	peroxisomal long-chain acyl-coA thioesterase
814353	0.4883684	phorbol-12-myristate-13-acetate-induced protein 1
897963	-1.0751021	phosphatidic acid phosphatase type 2A
346942	0.5326646	phosphatidylinositol glycan, class Q
788136	-1.0073983	phosphodiesterase 4B, cAMP-specific ( <i>dunce</i> ( <i>Drosophila</i> )-homolog phosphodiesterase E4)
625923	0.7725056	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
712401	-1.193113	phosphoinositide-3-kinase, catalytic, delta polypeptide
811142	0.4595393	phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)
272529	0.8371698	phosphomannomutase 2
725284	0.6014099	phosphorylase kinase, gamma 2 (testis)
1474337	-0.986117	phosphorylase, glycogen; brain
843195	0.86501	phosphoserine phosphatase
503215	0.9757636	pilin-like transcription factor
810124	0.9124035	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
365358	0.696963	pM5 protein
290378	-1.2346086	podocalyxin-like
859761	0.8563964	poliovirus receptor-related 2 (herpesvirus entry mediator B)
744047	0.4802334	polo ( <i>Drosophila</i> )-like kinase
897813	0.5034689	polyadenylate binding protein-interacting protein 1
741769	0.5565863	polymerase (DNA directed), beta
810734	0.6603412	polymerase (DNA-directed), delta 4
813410	0.5664086	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
1325816	0.6742078	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
2063982	0.4651856	potassium channel, subfamily K, member 6 (TWIK-2)
756708	-1.1346161	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4
67741	-1.4786722	PP2135 protein

69002 -1.3581187 PPAR(gamma) angiopoietin related protein  
241348 0.8182422 prenylcysteine lyase  
280375 0.9155003 PRO2000 protein  
2020898 0.6044163 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3  
826173 0.4276784 profilin 1  
486110 0.5127183 profilin 2  
41698 0.4938629 progesterone binding protein  
837864 0.4345283 progestin induced protein  
1573946 0.5875624 programmed cell death 9  
138788 0.6497728 prolactin receptor  
855800 0.6235647 prolyl endopeptidase  
27544 -0.9834143 prominin (mouse)-like 1  
810558 0.9227709 proteasome (prosome, macropain) 26S subunit, ATPase, 4  
2050827 0.7156518 proteasome (prosome, macropain) 26S subunit, ATPase, 5  
1553306 0.6066787 proteasome (prosome, macropain) 26S subunit, non-  
ATPase, 11  
823598 0.9452282 proteasome (prosome, macropain) 26S subunit, non-  
ATPase, 12  
2054635 0.831532 proteasome (prosome, macropain) subunit, alpha type, 7  
122241 0.7352191 proteasome (prosome, macropain) subunit, beta type, 2  
951233 0.7240615 proteasome (prosome, macropain) subunit, beta type, 3  
1460110 0.6397172 proteasome (prosome, macropain) subunit, beta type, 5  
1473289 0.7441483 protective protein for beta-galactosidase (galactosialidosis)  
26883 0.4176151 protein kinase (cAMP-dependent, catalytic) inhibitor beta  
755301 0.5790795 protein kinase C, delta  
2055807 0.6216372 protein kinase domains containing protein similar to  
phosphoprotein C8FW  
205049 0.6682666 protein kinase H11; small stress protein-like protein HSP22  
756666 0.6269882 protein phosphatase 1, catalytic subunit, alpha isoform  
814989 0.4419384 protein phosphatase 1G (formerly 2C), magnesium-  
dependent, gamma isoform  
41356 0.5683316 protein phosphatase 2, regulatory subunit B (B56), alpha  
isoform  
358162 0.616765 protein predicted by clone 23627  
785707 0.5133005 protein regulator of cytokinesis 1

774502	0.4222849	protein tyrosine phosphatase, non-receptor type 12
151449	0.4189856	protein tyrosine phosphatase, non-receptor type 21
83363	0.748646	protein-L-isoaspartate (D-aspartate) O-methyltransferase
145491	0.4250102	protocadherin 1 (cadherin-like 1)
303109	-1.2557454	purinergic receptor (family A group 5)
141852	0.5762886	purinergic receptor P2Y, G-protein coupled, 2
1917941	0.9960315	purine-rich element binding protein B
744374	0.6732551	putative ankyrin-repeat containing protein
685516	0.8694652	putative G protein-coupled receptor
122077	1.2356703	putative membrane protein
261472	0.6215341	putative nuclear protein ORF1-FL49
795498	0.5557245	putative transmembrane protein
826077	0.5405591	pyruvate dehydrogenase (lipoamide) beta
365060	0.5244569	RAB11A, member RAS oncogene family
79520	0.6919579	RAB2, member RAS oncogene family
741891	0.4775456	RAB2, member RAS oncogene family-like
1911343	0.967716	RAB26, member RAS oncogene family
1639531	0.6315732	RAB27A, member RAS oncogene family
784150	0.5598483	RAB31, member RAS oncogene family
785701	0.7413837	RAB31, member RAS oncogene family
1845169	0.8033348	RAB35, member RAS oncogene family
470124	0.7539249	RAD1 ( <i>S. pombe</i> ) homolog
1476053	0.6522237	RAD51 ( <i>S. cerevisiae</i> ) homolog (E coli RecA homolog)
505864	-1.2393277	RalGDS-like gene
143426	0.5173212	ras homolog gene family, member B
45099	-1.6325981	regucalcin (senescence marker protein-30)
2106144	-1.1619925	regulated in glioma
1500542	0.5032679	regulator of G-protein signalling 11
813707	0.6252347	regulator of G-protein signalling 16
2017403	0.5117711	regulator of G-protein signalling 3
781097	0.7633668	reticulon 3
2322367	0.7249854	reticulon 4
595037	1.3057353	retinoic acid induced 3
812994	0.671102	retinoid X receptor, alpha
810959	0.505619	Rho GDP dissociation inhibitor (GDI) alpha
244801	1.0162794	Rho guanine exchange factor (GEF) 11
756373	0.4310628	Rho guanine exchange factor (GEF) 16
1422338	0.5652946	ribonucleotide reductase M2 polypeptide
990881	-1.0289558	<b>ribosomal protein L12 (Rpl12), mus musculus</b>

814316	-1.0654718	ribosomal protein L13
123441	0.7124698	ribosomal protein L7a
772898	0.520392	ribosomal protein S15a
469686	0.9203022	Ric ( <i>Drosophila</i> )-like, expressed in many tissues
1636844	0.4627748	ring finger protein 14
133236	-1.0945253	RNA binding motif protein, X chromosome
291478	-1.3155899	runt-related transcription factor 3
756595	0.5433619	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
810612	0.842284	S100 calcium-binding protein A11 (calgizzarin)
824108	0.4369933	SCAN domain-containing 1
416434	-1.0284229	SCN Circadian Oscillatory Protein (SCOP)
785840	0.4219115	SEC24 ( <i>S. cerevisiae</i> ) related gene family, member D
2306987	0.4670155	secreted and transmembrane 1
878836	-1.2507242	secretory granule, neuroendocrine protein 1 (7B2 protein)
840878	0.6216124	seladin-1
1492463	1.087152	selenoprotein X, 1
592801	0.4785497	serine palmitoyltransferase, long chain base subunit 2
814378	0.6857148	serine protease inhibitor, Kunitz type, 2
209066	0.7693907	serine/threonine kinase 15
209066	0.8120797	<b>serine/threonine kinase 15</b>
161456	-0.9820939	serum amyloid A1
1917449	-1.1785893	serum amyloid A4, constitutive
470061	0.9665514	seven in absentia ( <i>Drosophila</i> ) homolog 2
813631	0.5754418	seven transmembrane protein TM7SF3
49351	0.75115	SEX gene
343760	-0.9907562	SH3 domain binding glutamic acid-rich protein like 2
2302099	0.7117055	sialidase 3 (membrane sialidase)
813751	0.7659116	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)
785616	0.7131593	signal sequence receptor, alpha (translocon-associated protein alpha)
2504881	-1.0194516	signal transducer and activator of transcription 5A
144740	0.630134	similar to phosphatidylcholine transfer protein 2
140574	-1.2754214	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)

2322223 0.5047814 small nuclear ribonucleoprotein polypeptide A  
704414 0.8520508 small nuclear ribonucleoprotein polypeptides B and B1  
288999 0.9896012 small protein effector 1 of Cdc42  
1692195 0.4471181 smg GDS-ASSOCIATED PROTEIN  
530958 -1.0316423 smoothened (*Drosophila*) homolog  
810762 0.5072899 SNARE protein  
472103 0.503987 soc-2 (suppressor of clear, *C.elegans*) homolog  
810875 0.4176896 solute carrier family 26, member 6  
49273 0.742123 solute carrier family 27 (fatty acid transporter), member 4  
782689 0.4570254 solute carrier family 6 (neurotransmitter transporter, creatine), member 8  
1702742 0.453453 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5  
773286 0.5158979 solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1  
76362 0.4553121 spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)  
1734309 0.6672454 sperm associated antigen 4  
503866 0.4884193 sperm autoantigenic protein 17  
565235 0.4428854 spermine synthase  
124781 0.5832065 squalene epoxidase  
1558675 -1.6577507 SRY (sex determining region Y)-box 10  
1469425 0.9610542 SRY (sex determining region Y)-box 22  
768571 -1.1461886 SRY (sex determining region Y)-box 8  
25440 0.4304195 staufen (*Drosophila*, RNA-binding protein) homolog 2  
2018084 0.6822251 Ste-20 related kinase  
302031 0.6626629 Ste20-related serine/threonine kinase  
810711 0.869424 stearoyl-CoA desaturase (delta-9-desaturase)  
.590759 0.5791873 sterol-C4-methyl oxidase-like  
35191 0.4165847 stromal cell-derived factor 2  
366132 1.1911439 succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD  
781014 -1.2359239 suppression of tumorigenicity 5  
969877 0.8382113 synaptosomal-associated protein, 25kD  
177827 0.4500254 synaptotagmin VII  
826194 0.5486839 synaptotagmin-like 2  
135640 0.4708685 syntaxin 3A  
509588 0.49319 TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD

1474955	0.8460414	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
726637	0.45959	t-complex-associated-testis-expressed 1-like
346696	0.5838269	TEA domain family member 4
47043	-1.0559861	tensin
795543	0.4364791	thioredoxin peroxidase (antioxidant enzyme)
965223	0.4687291	thymidine kinase 1, soluble
739126	0.6881663	tissue specific transplantation antigen P35B
825470	0.5523318	topoisomerase (DNA) II alpha (170kD)
1591264	0.5440944	transaldolase 1
347373	0.8555396	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)
823940	0.4997308	transducer of ERBB2, 1
705064	0.5238148	transforming, acidic coiled-coil containing protein 3
882248	-0.9965858	transgelin
359887	1.052326	translocase of inner mitochondrial membrane 17 (yeast) homolog A
149355	0.6943923	translocating chain-associating membrane protein
826256	0.8700831	transmembrane 7 superfamily member 1 (upregulated in kidney)
298417	0.4235025	trefoil factor 3 (intestinal)
855749	0.5432466	triosephosphate isomerase 1
740620	-1.0395569	tropomyosin 2 (beta)
611532	-1.273871	troponin I, skeletal, fast
1409509	0.7370811	troponin T1, skeletal, slow
489657	0.4609514	tryptophan rich basic protein
757489	0.5386267	tubulin, alpha 2
825585	0.6413235	tubulin-specific chaperone e
491403	-1.0411657	tumor necrosis factor receptor superfamily, member 1B
814306	0.630078	tumor protein D52
1435003	0.8098225	tumor suppressing subtransferable candidate 1
1856063	-1.0036618	tweety (Drosophila) homolog 1
292996	0.5341429	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
868396	-0.9916319	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
626318	0.4746692	ubinuclein 1
769921	0.726646	ubiquitin carrier protein E2-C

81599	0.5067033	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)
1698036	0.5843382	ubiquitin-conjugating enzyme E2 variant 1
839682	0.5542571	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
289978	0.6090234	ubiquitin-like 4
713862	0.4400704	ubiquitin-protein isopeptide ligase (E3)
824524	0.5296138	UDP-galactose transporter related
139835	0.5590106	UDP-glucose dehydrogenase
809727	0.4224266	unc-51 ( <i>C. elegans</i> )-like kinase 1
284261	0.7445419	uncharacterized hematopoietic stem/progenitor cells protein MDS030
884498	0.5640535	uncharacterized hypothalamus protein HT012
236034	0.9534619	uncoupling protein 2 (mitochondrial, proton carrier)
783681	0.4412503	upstream regulatory element binding protein 1
769600	0.5106262	uracil-DNA glycosylase 2
81336	0.6099072	uteroglobin
1631699	0.6665952	valosin-containing protein
855563	0.5987092	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3
810316	0.4245985	very long-chain acyl-CoA synthetase; lipidosin
71087	-1.2181178	v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F
322617	0.5188645	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
784140	0.6102245	WD repeat domain 15
731023	0.7151176	WD repeat domain 5
268946	0.4751692	WD40 protein Ciao1
2306221	0.4385881	wingless-type MMTV integration site family, member 10B
235986	0.5649127	wingless-type MMTV integration site family, member 11
138189	1.0692241	Wolfram syndrome 1 (wolframin)
813281	0.9107661	WW domain-containing protein 1
795185	0.9295627	xenotropic and polytropic retrovirus receptor
813629	0.7288266	YME1 ( <i>S.cerevisiae</i> )-like 1
209537	-0.9988461	zinc finger protein 221

Table 3 (in alphabetical order)

CloneID	Weight	Description
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1574058	0.6261947	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
73252	-0.6115602	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
725076	-0.6798005	5'-nucleotidase (purine), cytosolic type B
1902764	-0.5683052	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
2325804	0.5840656	95 kDa retinoblastoma protein binding protein
713782	0.5273402	a disintegrin and metalloproteinase domain 15 (metarginin)
1738208	0.7166687	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4
488505	0.4727394	accessory proteins BAP31/BAP29
1587863	0.7507482	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
855029	0.4904632	Ac-like transposable element
279970	0.5992634	adenosine A2a receptor
712139	-1.2371074	ADP-ribosylation factor-like 7
814798	-0.9611553	aldehyde dehydrogenase 1 family, member A3
47853	0.6077928	aldehyde dehydrogenase 4 family, member A1
196992	-0.6573113	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
23831	-0.8493217	aldolase C, fructose-bisphosphate
272706	-0.7274769	alpha2,3-sialyltransferase
1635320	-0.8845852	amiloride-sensitive cation channel 2, neuronal
809998	-0.5519459	amylase, alpha 2A; pancreatic
2250839	0.654954	androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
2019101	0.4289318	angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8)
344854	-0.692296	ankyrin repeat domain 3
208718	-0.7660278	annexin A1
666879	-0.7950485	annexin A8
239568	0.5750382	annexin A9
1435862	0.8934643	antigen identified by monoclonal antibodies 12E7, F21 and O13
2110511	0.6203153	artemin
183440	0.4967506	arylsulfatase A

815737 -1.1857965 ATP synthase, H<sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle

266312 0.6856592 ATPase, Cu<sup>++</sup> transporting, beta polypeptide (Wilson disease)

840768 0.4812559 ATPase, H<sup>+</sup> transporting, lysosomal (vacuolar proton pump) 16kD

810725 0.51329 ATPase, H<sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD

156211 -0.8269263 ATPase, H<sup>+</sup> transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 1 (Renal tubular acidosis with deafness)

48518 -0.6455041 ATP-binding cassette, sub-family A (ABC1), member 5

813256 -0.7334866 ATP-binding cassette, sub-family B (MDR/TAP), member 1

1558108 0.5577768 ATP-binding cassette, sub-family C (CFTR/MRP), member 8

767798 0.7682106 ATX1 (antioxidant protein 1, yeast) homolog 1

1709791 0.740832 BAI1-associated protein 1

1609665 -0.7765472 BarH-like homeobox 2

1558151 0.4723511 basic leucine zipper transcription factor, ATF-like

342181 0.557997 B-cell CLL/lymphoma 2

1456701 0.5545861 B-cell CLL/lymphoma 9

2244196 0.5432772 B-cell receptor-associated protein BAP29

1916575 0.5127478 BCL2-interacting killer (apoptosis-inducing)

809357 0.571929 Bernardinelli-Seip congenital lipodystrophy 2 (seipin)

878798 -0.5956349 beta-2-microglobulin

786069 -0.6484842 beta-site APP-cleaving enzyme

741977 0.6758385 B-factor, properdin

1733262 0.5891897 BLU protein

293964 -0.7275302 butyrophilin, subfamily 3, member A1

271472 0.6582514 C3HC4-like zinc finger protein

1601845 -0.7178673 Ca<sup>2+</sup>-promoted Ras inactivator

773301 -0.5147295 cadherin 3, type 1, P-cadherin (placental)

841679 0.6283163 calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)

772913 -0.9823487 calreticulin

359250 0.5382989 carbonic anhydrase IV

753301 -0.8393651 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)

744417 0.6563238 carnitine acetyltransferase

120106 -0.631375 caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)  
341763 -0.5868818 caspase 5, apoptosis-related cysteine protease  
72778 -0.6614808 caspase 7, apoptosis-related cysteine protease  
51083 0.5170561 catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)  
377461 -0.7093974 caveolin 1, caveolae protein, 22kD  
1946448 -0.790849 caveolin 2  
1572298 -0.5126426 CD3Z antigen, zeta polypeptide (TiT3 complex)  
739193 -0.7338774 cellular retinoic acid-binding protein 1  
1626996 -0.5573507 c-fos induced growth factor (vascular endothelial growth factor D)  
811774 0.7223819 CGI-49 protein  
221846 -0.5714352 checkpoint suppressor 1  
283023 -0.6577611 chemokine (C-X3-C) receptor 1  
79629 -0.6849525 **chemokine (C-X-C motif) receptor 4 (CXCR4), Homo sapiens**  
293569 0.8708985 chromosome 1 open reading frame 21  
742562 -0.9269494 chromosome 16 open reading frame 5  
1492426 0.4635224 chromosome 19 open reading frame 3  
490414 -0.6078858 chromosome 2 open reading frame 2  
824052 1.034408 chromosome 6 open reading frame 1  
144924 -0.5498123 chromosome 6 open reading frame 5  
50562 0.5195335 chromosome 8 open reading frame 4  
811149 -0.5319742 chromosome 9 open reading frame 3  
731308 0.6259858 citrate synthase  
1656062 0.4288838 coagulation factor XII (Hageman factor)  
85634 -0.5410684 complement component 1, s subcomponent  
  
77972 -0.5144916 complement component 3  
868652 0.4682053 complement component 4B  
809838 0.4466933 **contig C013216, human**  
127646 0.5663395 **contig C030249, human**  
360778 0.4820033 **contig C054624, human**  
177665 -0.5718286 **contig C055081, human**  
33267 0.6679827 **contig C064722, human**  
839736 -1.1019142 crystallin, alpha B  
1555924 -0.9421074 CSR1 protein  
488956 -0.6682156 CUG triplet repeat, RNA-binding protein 2  
701751 0.6961443 cut (Drosophila)-like 1 (CCAAT displacement protein)  
  
742595 0.6324947 cyclin-dependent kinase 5  
757873 -1.0188169 cyclin-dependent kinase 5, regulatory subunit 1 (p35)

2009491 -0.5334821 cyclin-E binding protein 1  
949938 0.5011384 cystatin C (amyloid angiopathy and cerebral hemorrhage)  
  
1323448 1.3237504 cysteine-rich protein 1 (intestinal)  
360254 -0.6612871 cysteine-rich, angiogenic inducer, 61  
196189 0.7992668 cytochrome b-5  
2013178 -1.0884449 death associated transcription factor 1  
2018423 -0.6275903 death-associated protein kinase 2  
756847 -0.5632582 deformed epidermal autoregulatory factor 1 (Drosophila)  
  
296702 0.5164562 deiodinase, iodothyronine, type I  
1492468 0.4643107 DEME-6 protein  
563634 -0.5737239 dendritic cell protein  
1161564 -0.8865787 desmuslin  
705274 0.4904221 diacylglycerol kinase, delta (130kD)  
760299 -0.8251086 dickkopf (Xenopus laevis) homolog 3  
35828 -0.5391332 diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)  
742685 -0.852598 disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)  
767761 0.4565666 DKFZP434B168 protein  
454970 -0.6853932 DKFZP434G032 protein  
366353 0.9154768 DKFZP564C186 protein  
770766 0.600234 DKFZP564C1940 protein  
294397 0.505999 DKFZP586A0522 protein  
767068 -0.6819032 DKFZP586G1517 protein  
202514 0.4902228 DNA (cytosine-5-)methyltransferase 3 alpha  
  
263727 0.5926363 DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)  
1876217 -0.5108977 DnaJ (Hsp40) homolog, subfamily A, member 2  
  
2018527 0.5732092 dolichyl-phosphate mannosyltransferase polypeptide 3  
  
884462 -0.9065675 Down syndrome critical region gene 1  
782688 0.4780253 dynein, axonemal, light intermediate polypeptide  
  
1864302 -0.6943806 E74-like factor 5 (ets domain transcription factor)  
  
840944 -0.6399619 early growth response 1  
781017 -0.5676944 early growth response 2 (Krox-20 (Drosophila) homolog)  
431231 -0.6692022 EGF-containing fibulin-like extracellular matrix protein 2  
  
188335 -0.7002579 egf-like module containing, mucin-like, hormone receptor-like sequence 2

2248488 0.7033736 ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate))  
  
74070 0.5225238 endosulfine alpha  
1693357 0.4274493 endothelin 2  
153760 -0.5361176 EphB1  
813520 -0.5889772 EphB3  
811088 -0.5445374 ephrin-B3  
1577736 -1.076549 epidermal growth factor (beta-urogastrone)  
504927 -0.5894078 epithelial protein up-regulated in carcinoma, membrane associated protein 17  
  
34093 -0.5692081 EST  
594500 1.158305 EST  
1641894 0.5187462 EST  
725321 0.44288 estrogen receptor 1  
27769 -0.5501268 ESTs  
34150 -0.5673709 ESTs  
40027 -0.6418674 ESTs  
75078 -0.7028415 ESTs  
83358 0.5709886 ESTs  
138672 -0.5483104 ESTs  
139660 -0.79833 ESTs  
162308 -0.6580605 ESTs  
196435 -0.653913 ESTs  
197056 -0.5440514 ESTs  
281190 -0.5572026 ESTs  
345032 0.4360992 ESTs  
415816 -0.5750184 ESTs  
462939 -0.5200097 ESTs  
470148 -0.5393193 ESTs  
490965 0.4389746 ESTs  
544639 -0.9767278 ESTs  
725622 -0.6731681 ESTs  
757191 -0.5735888 ESTs  
767706 0.4731085 ESTs  
814209 0.6076904 ESTs  
839580 0.4826315 ESTs  
1031640 -0.5354869 ESTs  
1257131 -0.8069059 ESTs  
1517749 0.947675 ESTs  
1557637 0.4588694 ESTs  
1558212 -0.5458261 ESTs  
1558233 0.7654043 ESTs  
1577920 -0.5161377 ESTs  
1880885 -0.5638973 ESTs

1883327 -0.5684295 ESTs  
1909935 -0.5368632 ESTs  
1911663 -0.5610314 ESTs  
289760 -0.7058375 ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]  
279720 0.6607182 ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]  
725978 0.5108817 ESTs, Moderately similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]  
530197 0.8206765 ESTs, Moderately similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]  
345670 -1.135654 ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]  
529843 -0.7117107 ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]  
289505 0.4933344 ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]  
179212 0.6499845 ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]  
3172883 -0.8293392 ESTs, Weakly similar to 1709359A dopamine D4 receptor [H.sapiens]  
160192 -0.5482009 ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]  
730313 0.5887579 ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]  
726699 0.4658249 ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]  
770848 -0.5188717 ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]  
128695 0.608873 ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]  
344073 0.4726399 ESTs, Weakly similar to K1Cl\_HUMAN KERATIN, TYPE I CYTOSKELETAL 9 [H.sapiens]  
950355 -0.550114 ESTs, Weakly similar to S13495 pregnancy zone protein [H.sapiens]  
35147 0.6842172 ESTs, Weakly similar to unnamed protein product [H.sapiens]

488202 0.5378254 ESTs, Weakly similar to YZ28\_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]

796542 -0.9052403 ets variant gene 5 (ets-related molecule)

301122 0.6041028 extracellular matrix protein 1

741139 -1.1025542 eyes absent (Drosophila) homolog 2

1469148 0.5125351 FGFR1 oncogene partner

752631 0.4426961 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)

812143 0.4519186 fibronectin leucine rich transmembrane protein 3

131839 -0.959265 folate receptor 1 (adult)

628955 -0.6088522 forkhead box O1A (rhabdomyosarcoma)

796475 -0.5563457 four and a half LIM domains 3

52419 -0.6326767 Friedreich ataxia region gene X123

298122 -0.8158372 frizzled (Drosophila) homolog 7

183200 0.4955056 fumarylacetoacetate hydrolase (fumarylacetoacetate)

2016775 -0.7914834 G protein-coupled receptor, family C, group 5, member B

209137 -0.6161588 gamma-aminobutyric acid (GABA) A receptor, epsilon

183556 0.4452493 gap junction protein, alpha 4, 37kD (connexin 37)

214068 0.5357344 GATA-binding protein 3

344959 0.8945717 gene for serine/threonine protein kinase

767495 0.4922026 GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)

1708055 0.554593 glioblastoma overexpressed

2018337 0.5163293 glucosidase, beta; acid (includes glucosylceramidase)

1609836 0.898716 glutamate-ammonia ligase (glutamine synthase)

504791 -0.6537859 glutathione S-transferase A4

344720 -0.8822302 glycophorin C (Gerbich blood group)

358217 0.6801945 glypican 4

811582 0.690137 golgi phosphoprotein 2

739578 0.5402953 GPI-anchored metastasis-associated protein homolog

132637 -0.5694152 grancalcin, EF-hand calcium-binding protein

713129 -0.5822078 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)

323238 -0.6032171 GRO1 oncogene (melanoma growth stimulating activity, alpha)

1556433 -0.7877792 GRO3 oncogene

40299 -0.78007 growth differentiation factor 10

788654 0.7336359 **growth factor receptor-bound protein 2**

788654	0.9585887	growth factor receptor-bound protein 2
810063	0.630827	growth factor, erv1 ( <i>S. cerevisiae</i> )-like (augmenter of liver regeneration)
51741	0.5094912	GTP-binding protein
767765	-0.5282008	GTP-binding protein overexpressed in skeletal muscle
308466	0.4417728	GTP-binding protein Sara
122394	0.5554851	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)
360518	-0.5253745	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1
1500000	0.5871787	H2B histone family, member B
40021	-0.5240809	hairless protein (putative single zinc finger transcription factor protein, responsible for autosomal recessive universal congenital alopecia, HR gene)
1870305	-0.5558155	heat shock 27kD protein 2
471568	0.5255851	hematological and neurological expressed 1
1569187	-0.7091259	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
1486082	-0.6241275	heparin-binding growth factor binding protein
488422	0.4626549	high-mobility group 20B
202577	0.5629317	histamine N-methyltransferase
611481	-0.7507264	HMG-box transcription factor TCF-3
2014373	0.8820247	HNK-1 sulfotransferase
1592715	0.4417898	Homer, neuronal immediate early gene, 3
782460	-0.5988226	<i>Homo sapiens</i> cDNA FLJ10500 fis, clone NT2RP2000369
171912	0.5297738	<i>Homo sapiens</i> cDNA FLJ10960 fis, clone PLACE1000564
854763	0.5918867	<i>Homo sapiens</i> cDNA FLJ11341 fis, clone PLACE1010786
825356	-0.5850287	<i>Homo sapiens</i> cDNA FLJ11997 fis, clone HEMBB1001458
186301	0.5537115	<i>Homo sapiens</i> cDNA FLJ12924 fis, clone NT2RP2004709
825327	0.4497029	<i>Homo sapiens</i> cDNA FLJ14105 fis, clone MAMMA1001202
503671	-1.1528584	<i>Homo sapiens</i> cDNA FLJ14368 fis, clone HEMBA1001122
488130	-0.5201845	<i>Homo sapiens</i> cDNA FLJ20767 fis, clone COL06986
241066	-0.5369493	<i>Homo sapiens</i> cDNA: FLJ21028 fis, clone CAE07155
823615	0.471739	<i>Homo sapiens</i> cDNA: FLJ21245 fis, clone COL01184

1541711 0.4694413 Homo sapiens cDNA: FLJ21513 fis, clone COL05778  
131094 0.6268883 Homo sapiens cDNA: FLJ21587 fis, clone COL06946  
812256 -0.5832398 Homo sapiens cDNA: FLJ21693 fis, clone COL09609  
810097 -0.5423072 Homo sapiens cDNA: FLJ21721 fis, clone COLF0381  
70749 -0.5295091 Homo sapiens cDNA: FLJ21874 fis, clone HEP02488  
1500815 -0.6008126 Homo sapiens cDNA: FLJ22130 fis, clone HEP19632  
814528 0.6329458 Homo sapiens cDNA: FLJ22139 fis, clone HEP20959  
731459 0.4427978 Homo sapiens cDNA: FLJ22296 fis, clone HRC04468  
753071 -1.4473398 Homo sapiens cDNA: FLJ22528 fis, clone HRC12825  
782537 0.490998 Homo sapiens cDNA: FLJ22562 fis, clone HSI01814  
840266 -0.9425178 Homo sapiens cDNA: FLJ22667 fis, clone HSI08385  
726703 0.5118991 Homo sapiens clone 23736 mRNA sequence  
898222 0.8092364 Homo sapiens clone 24418 mRNA sequence  
491519 -0.5282605 Homo sapiens clone 24775 mRNA sequence  
796723 0.576028 Homo sapiens clone CDABP0014 mRNA sequence  
488404 -0.6521658 Homo sapiens clone TUA8 Cri-du-chat region mRNA  
752837 -0.6056177 Homo sapiens mRNA for FLJ00074 protein, partial cds  
745011 -0.5836864 Homo sapiens mRNA for KIAA1750 protein, partial cds  
70245 -0.6422928 Homo sapiens mRNA full length insert cDNA clone  
EUROIMAGE 50374  
970590 -0.5383645 Homo sapiens mRNA; cDNA DKFZp434A115 (from clone  
DKFZp434A115)  
24958 -0.5349519 Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone  
DKFZp434C2016)  
590310 0.6299822 Homo sapiens mRNA; cDNA DKFZp434E2321 (from clone  
DKFZp434E2321); partial cds  
137602 -0.5667198 Homo sapiens mRNA; cDNA DKFZp434G0972 (from clone  
DKFZp434G0972)

265103 0.702883 Homo sapiens mRNA; cDNA DKFZp547M123 (from clone DKFZp547M123)  
565319 0.6603668 Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)  
813265 -0.7192289 Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)  
486683 -1.0075654 Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)  
504959 0.5953946 Homo sapiens mRNA; cDNA DKFZp586G0321 (from clone DKFZp586G0321)  
22917 -0.7173328 Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)  
823727 0.4406546 Homo sapiens, clone IMAGE:2905978, mRNA, partial cds  
782497 0.5218113 Homo sapiens, clone IMAGE:3010666, mRNA, partial cds  
1631735 0.5228778 Homo sapiens, clone IMAGE:3604336, mRNA, partial cds  
186768 0.6495706 Homo sapiens, clone IMAGE:3604869, mRNA  
292770 0.4944242 Homo sapiens, clone IMAGE:3627860, mRNA, partial cds  
1652310 0.4525789 Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds  
810002 -1.2720931 Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds  
130835 0.8659688 Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA  
588262 0.5614929 Homo sapiens, Similar to RIKEN cDNA 2600001A11 gene, clone MGC:9907 IMAGE:3870073, mRNA, complete cds  
1649374 0.5731982 homogentisate 1,2-dioxygenase (homogentisate oxidase)  
839081 0.4939384 homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2  
2017756 0.4608709 homolog of yeast MOG1  
1492238 0.9155471 HSPC003 protein

178805 0.8524069 Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to Drosophila Scratch (Scrt), Slug and Xenopus Snail, a novel gene similar to Drosophila CG6762, STSs, GSSs and five CpG

813419 0.5602324 hydroxyacyl-Coenzyme A dehydrogenase, type II

768007 -0.547374 hypothetical protein

810402 0.4583168 hypothetical protein

811848 -0.5637994 hypothetical protein

825822 0.5134094 hypothetical protein

1734754 -0.5512835 hypothetical protein B

32489 -0.7521767 hypothetical protein DKFZp566A1524

76182 -0.6603322 hypothetical protein DKFZp761F241

725152 -0.7173869 hypothetical protein DKFZp762A227

842896 -0.8123068 hypothetical protein DKFZp762L0311

491465 0.4821169 hypothetical protein FLJ10035

503889 0.4433034 hypothetical protein FLJ10656

233349 0.6764709 hypothetical protein FLJ10761

41869 -0.7646494 hypothetical protein FLJ11017

126851 0.5535041 hypothetical protein FLJ11160

489106 0.4628623 hypothetical protein FLJ11210

768570 0.6581316 hypothetical protein FLJ11280

84464 -0.6091345 hypothetical protein FLJ12806

785733 -0.7554682 hypothetical protein FLJ12892

156363 0.5086284 hypothetical protein FLJ12934

1605426 0.5150013 hypothetical protein FLJ13352

796498 -0.5900328 hypothetical protein FLJ14007

43764 -0.6743049 hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit

1554167 -0.7503289 hypothetical protein FLJ14529

250797 -0.7739669 hypothetical protein FLJ20038

1505038 0.43988 hypothetical protein FLJ20171

1881689 -0.568518 hypothetical protein FLJ20281

502774 0.5204735 hypothetical protein FLJ20623

1636092 0.4404649 hypothetical protein FLJ20657

810981 0.498146 hypothetical protein FLJ20699

300632 -0.8586688 hypothetical protein FLJ21044 similar to Rbig1

37671 -0.5712258 hypothetical protein FLJ21610

1636156 -0.7827089 hypothetical protein FLJ21709

1470278 -0.5449844 hypothetical protein FLJ21841

811907 0.6180993 hypothetical protein FLJ22056

767456 -0.5555493 hypothetical protein FLJ22167

1493218 -0.6292715 hypothetical protein FLJ22297

1947381	0.4311314	hypothetical protein FLJ22329
37554	0.6440792	hypothetical protein FLJ22353
1417886	-0.563564	hypothetical protein FLJ23239
220395	-0.7687195	hypothetical protein FLJ23293 similar to ARL-6 interacting protein-2
743146	0.6388187	hypothetical protein FLJ23403
509458	-0.5266016	hypothetical protein from clone 643
292388	-0.554297	<b>hypothetical protein MAC30 (MAC30), Homo sapiens</b>
1609748	0.4955206	hypothetical protein MGC10882
824879	0.5548666	hypothetical protein MGC11275
68636	0.7904354	hypothetical protein MGC2477
770869	0.4762758	hypothetical protein MGC2592
490023	-0.7621736	hypothetical protein MGC2648
1558642	0.4426424	hypothetical protein MGC2771
773142	0.4530754	hypothetical protein MGC2827
773487	-0.6598647	hypothetical protein MGC3032
37708	0.5283276	hypothetical protein MGC3101
814443	-0.5075293	hypothetical protein MGC3232
1570427	-0.601608	hypothetical protein MGC4309
42408	0.5930231	hypothetical protein MGC4604
123614	0.4800042	hypothetical protein MGC4675
120271	0.4425879	hypothetical protein MGC4692
812238	0.5237287	hypothetical protein MGC4692
1858892	0.5295858	hypothetical protein MGC4825
745606	0.8514931	hypothetical protein PP591
1704155	-0.5133015	hypothetical protein SBBI48
840677	-0.5611985	immunoglobulin kappa constant
39884	0.5659552	IMP (inosine monophosphate) dehydrogenase 1
788234	-1.0610946	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
505243	-0.5616577	inositol 1,4,5-triphosphate receptor, type 2
703964	-0.5918604	inositol polyphosphate phosphatase-like 1
180803	-0.5083354	inositol polyphosphate-1-phosphatase
32299	-0.5945347	inositol(myo)-1(or 4)-monophosphatase 2
502436	-0.5489864	insulin receptor substrate 2
814350	0.6173648	insulin-degrading enzyme
471196	-0.7192752	integral membrane protein 3
32493	-0.9043423	integrin, alpha 6
130201	-0.5468031	intercellular adhesion molecule 2
824602	-0.5965816	interferon, gamma-inducible protein 16
856447	0.494183	interferon, gamma-inducible protein 30
811920	-0.8286379	interleukin 11 receptor, alpha
1517171	0.5204242	interleukin 2 receptor, alpha
120138	0.7096046	J domain containing protein 1

414992	0.5293379	K562 cell-derived leucine-zipper-like protein 1
809784	-0.6348991	kallikrein 6 (neurosin, zyme)
1474900	-0.5693091	keratin 15
415191	-0.700303	KIAA0161 gene product
812975	-0.6527728	KIAA0172 protein
1473471	-0.7906678	KIAA0194 protein
826668	0.550158	KIAA0274 gene product
1884404	0.4878341	KIAA0285 gene product
809944	0.4291762	KIAA0310 gene product
324927	-0.5284875	KIAA0375 gene product
826622	0.5532463	KIAA0430 gene product
754028	-0.5396001	KIAA0469 gene product
753162	-0.5377767	KIAA0603 gene product
1636166	-0.7788972	KIAA0668 protein
40173	0.5771304	KIAA0807 protein
460126	-0.5652362	KIAA0819 protein
1534700	-0.8804685	KIAA0830 protein
1901310	-0.5229967	KIAA1209 protein
345056	-0.6490368	KIAA1404 protein
665384	-0.7388404	KIAA1609 protein
1881774	-0.6332545	KIAA1678
149539	0.9878366	KIAA1700
277571	-0.59335	KIAA1706 protein
703541	-0.7118124	KIAA1858 protein
278430	0.4612914	kinesin family member 5C
753038	-1.1168529	kinesin family member C3
796539	-0.803124	KRAB-associated protein 1
488025	0.8525751	Kruppel-associated box protein
132711	-0.6985643	Kruppel-like factor 5 (intestinal)
795178	-0.5532479	lactate dehydrogenase C
346545	-0.6098367	laminin, beta 1
897731	-0.6548064	Iatrophilin
199403	0.6027193	lectin, galactoside-binding, soluble, 8 (galectin 8)
60565	0.5192032	lethal giant larvae (Drosophila) homolog 2
470092	0.5319336	like-glycosyltransferase
712829	-0.5181236	LIM domain only 2 (rhombotin-like 1)
783698	-0.7411614	lipin 1
247616	-0.5358709	lipoma HMGIC fusion partner
1469377	-0.9086679	lipoma HMGIC fusion partner-like 2
868169	-0.6224058	lipoprotein lipase
825296	0.4858551	low density lipoprotein receptor defect C complementing
490778	0.5957445	low molecular mass ubiquinone-binding protein (9.5kD)

341759 -0.7393558 lung type-I cell membrane-associated glycoprotein  
255754 0.7720883 LUNX protein; PLUNC (palate lung and nasal epithelium clone); tracheal epithelium enriched protein  
1470048 -0.5729078 lymphocyte antigen 6 complex, locus E  
341774 -0.7044768 major histocompatibility complex, class I, A  
2014856 0.5837779 major histocompatibility complex, class I-like sequence  
145132 0.6725186 mannose-P-dolichol utilization defect 1  
589115 0.531314 matrix metalloproteinase 1 (interstitial collagenase)  
470393 -0.848482 matrix metalloproteinase 7 (matrilysin, uterine)  
200814 -0.7920988 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)  
729975 0.5908615 meningioma expressed antigen 5 (hyaluronidase)  
1518890 0.4610867 metallothionein-like 5, testis-specific (tesmin)  
878406 0.4311455 metaxin 1  
79254 -0.541673 MHC class I region ORF  
1587847 -0.5466442 minichromosome maintenance deficient (mis5, *S. pombe*) 6  
1390584 0.4284863 mitochondrial intermediate peptidase  
788334 0.6264069 mitochondrial ribosomal protein L23  
417801 0.4325892 mitochondrial ribosomal protein L27  
782608 0.6105794 **mitochondrial ribosomal protein L9**  
782608 0.8041049 mitochondrial ribosomal protein L9  
771173 0.6594128 mitochondrial ribosomal protein S21  
70201 -0.7513314 mitochondrial solute carrier  
590774 0.6071935 mitogen-activated protein kinase 13  
2326057 0.4506179 MLN51 protein  
1075635 0.4502629 MLSN1- and TRP-related  
1420842 -0.5574834 mucosa associated lymphoid tissue lymphoma translocation gene 1  
450301 0.8030667 mutL (*E. coli*) homolog 3  
611443 0.6112713 myoglobin  
786072 0.5450231 myosin IC  
470128 -0.5652125 myosin IE  
66599 0.5399379 N-acetyltransferase 1 (arylamine N-acetyltransferase)  
1635681 0.5859113 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)  
487733 0.4356439 **NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)**

1762111	0.5703701	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
76605	0.5482232	nesca protein
838478	-0.934433	neurocalcin delta
2306697	0.4953741	neuromedin B
289428	-0.6542789	neurotrophic tyrosine kinase, receptor, type 2
877621	-0.8289253	nGAP-like protein
306798	-0.5742664	NGFI-A binding protein 1 (EGR1 binding protein 1)
75859	-1.6337267	N-myc downstream-regulated gene 2
726658	0.5132765	non-metastatic cells 3, protein expressed in
795256	0.4753832	NPD007 protein
754040	-0.5282144	NS1-associated protein 1
416959	-0.5999728	nuclear factor I/B
753034	-0.5182019	nuclear factor I/X (CCAAT-binding transcription factor)
725649	0.4878638	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
2710524	0.6399293	nuclear receptor coactivator 3
823714	-0.7215045	nuclear receptor co-repressor/HDAC3 complex subunit
843070	-0.8071984	nucleoporin 88kD
840882	0.441569	nucleotide binding protein
42681	-0.718704	NY-REN-25 antigen
66535	0.466705	ornithine decarboxylase antizyme 2
2028722	-0.5277252	osteoblast specific factor 2 (fasciclin I-like)
781019	0.5132896	paraoxonase 2
1404774	0.5399447	parathyroid hormone-like hormone
430318	0.4681908	parvalbumin
416676	-0.8568853	pellino ( <i>Drosophila</i> ) homolog 1
285377	-0.8214706	pellino ( <i>Drosophila</i> ) homolog 2
951125	0.4675003	peroxisomal D3,D2-enoyl-CoA isomerase
788518	-0.5724497	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)
289857	0.4823282	phenylethanolamine N-methyltransferase
1957136	0.5006732	phenylethanolamine N-methyltransferase
788136	-0.8998648	phosphodiesterase 4B, cAMP-specific ( <i>dunce</i> ( <i>Drosophila</i> )-homolog phosphodiesterase E4)
712401	-0.5107426	phosphoinositide-3-kinase, catalytic, delta polypeptide
33949	-0.5222135	phosphoribosyl pyrophosphate synthetase-associated protein 1
1474337	-0.844539	phosphorylase, glycogen; brain
503215	0.6457259	pilin-like transcription factor

810017 0.5135433 plasminogen activator, urokinase receptor  
66491 -0.5579872 plasmolipin  
796904 -0.604755 pleiomorphic adenoma gene-like 1  
365358 0.4756564 pM5 protein  
290378 -1.0043647 podocalyxin-like  
1474149 0.5138729 poliovirus receptor-related 1 (herpesvirus entry mediator C; nectin)  
859761 0.5582503 poliovirus receptor-related 2 (herpesvirus entry mediator B)  
741769 0.6390692 polymerase (DNA directed), beta  
810734 0.5308572 polymerase (DNA-directed), delta 4  
232789 0.4292025 polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)  
1325816 0.6829962 polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)  
756708 -0.9396531 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4  
1156538 0.7512287 potassium inwardly-rectifying channel, subfamily J, member 11  
2017960 -0.5822336 PP1201 protein  
67741 -0.7229251 PP2135 protein  
69002 -0.8528453 PPAR(gamma) angiopoietin related protein  
812048 -0.6438062 prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)  
284592 -0.9019931 PRO1659 protein  
1573946 0.509585 programmed cell death 9  
27544 -0.7342174 prominin (mouse)-like 1  
1456118 -0.7074166 proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2)  
1473289 0.4540707 protective protein for beta-galactosidase (galactosialidosis)  
756666 0.474441 protein phosphatase 1, catalytic subunit, alpha isoform  
786545 0.4453714 protein phosphatase 1, regulatory (inhibitor) subunit 3B  
151449 0.5503739 protein tyrosine phosphatase, non-receptor type 21  
303109 -0.6571713 purinergic receptor (family A group 5)  
685516 0.5304998 putative G protein-coupled receptor  
122077 0.434495 putative membrane protein  
261472 0.4814013 putative nuclear protein ORF1-FL49  
826077 0.503983 pyruvate dehydrogenase (lipoamide) beta  
810331 0.6014164 quiescin Q6  
23776 0.879215 quinoid dihydropteridine reductase

741891 0.7360507 RAB2, member RAS oncogene family-like  
1911343 0.559091 RAB26, member RAS oncogene family  
248886 -0.6161134 rab3 GTPase-activating protein, non-catalytic subunit (150kD)  
  
784150 0.4763599 RAB31, member RAS oncogene family  
785701 0.6496359 RAB31, member RAS oncogene family  
245296 -0.5184238 RAD52 (*S. cerevisiae*) homolog  
1686766 -0.5342051 Rag D protein  
505864 -0.7020337 RalGDS-like gene  
143426 0.4679928 ras homolog gene family, member B  
80727 -0.5766546 receptor tyrosine kinase-like orphan receptor 1  
  
45099 -0.5753698 regucalcin (senescence marker protein-30)  
  
1500542 0.5341753 regulator of G-protein signalling 11  
2017403 0.5568495 regulator of G-protein signalling 3  
595037 0.5870709 retinoic acid induced 3  
755689 -0.5122586 retinoic acid receptor, gamma  
244801 0.5693836 Rho guanine exchange factor (GEF) 11  
814316 -0.521831 ribosomal protein L13  
51078 -0.8348835 ribosomal protein L44  
133236 -0.7561129 RNA binding motif protein, X chromosome  
813845 0.6018909 RNA, U transporter 1  
26294 0.5137265 RNB6  
291478 -1.0093382 runt-related transcription factor 3  
810612 0.4352602 S100 calcium-binding protein A11 (calgizzarin)  
  
844703 -0.5309356 Sam68-like phosphotyrosine protein, T-STAR  
  
627248 0.4972176 SBBI31 protein  
814526 -0.5156162 seb4D  
378813 -0.679848 secretory leukocyte protease inhibitor (antileukoproteinase)  
  
1492463 0.8378401 selenoprotein X, 1  
207735 -0.5422739 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1  
  
531319 -0.5404527 serine/threonine kinase 12  
813631 0.4607567 seven transmembrane protein TM7SF3  
49351 0.4697521 SEX gene  
1603583 0.4785029 SH3 domain binding glutamic acid-rich protein like  
  
2302099 0.4967769 sialidase 3 (membrane sialidase)  
345034 -0.8161772 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)  
140574 -0.8498606 small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)

704414 0.5431136 small nuclear ribonucleoprotein polypeptides B and B1  
288999 0.5955672 small protein effector 1 of Cdc42  
530958 -0.5423532 smoothened (*Drosophila*) homolog  
2054122 0.698129 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3  
49273 0.4937997 solute carrier family 27 (fatty acid transporter), member 4  
782689 0.4930071 solute carrier family 6 (neurotransmitter transporter, creatine), member 8  
815142 -0.5782827 spastic ataxia of Charlevoix-Saguenay (sacsin)  
1558675 -1.4515145 SRY (sex determining region Y)-box 10  
1469425 0.6055267 SRY (sex determining region Y)-box 22  
768571 -0.7476813 SRY (sex determining region Y)-box 8  
2018084 0.4999242 Ste-20 related kinase  
302031 0.49677 Ste20-related serine/threonine kinase  
366132 0.5711651 succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD  
22778 0.6100322 sulfotranferase family 4A, member 1  
418159 -0.6038708 synaptogyrin 1  
969877 0.6064355 synaptosomal-associated protein, 25kD  
177827 0.5085582 synaptotagmin VII  
487932 0.4419815 synaptotagmin-like 2  
826194 0.6205287 synaptotagmin-like 2  
346696 0.437234 TEA domain family member 4  
363144 0.7924672 transcription factor AP-2 beta (activating enhancer-binding protein 2 beta)  
725680 -0.6295778 transcription factor AP-2 gamma (activating enhancer-binding protein 2 gamma)  
713839 -0.5088558 transcription factor AP-4 (activating enhancer-binding protein 4)  
868630 -0.5426831 transforming growth factor beta-stimulated protein TSC-22  
826256 0.6554059 transmembrane 7 superfamily member 1 (upregulated in kidney)  
298417 0.4587501 trefoil factor 3 (intestinal)  
740620 -0.5730915 tropomyosin 2 (beta)  
611532 -0.5320107 troponin I, skeletal, fast  
612274 -0.6108452 tubulin, alpha 1 (testis specific)  
142259 -0.7380151 tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntington interacting protein L; transcription factor IIIA-interacting protein  
491403 -0.6760814 tumor necrosis factor receptor superfamily, member 1B

1607229 -0.7562938 tumor protein D52-like 1  
1856063 -0.5866417 tweety (*Drosophila*) homolog 1  
868396 -0.6426678 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide  
150897 -1.0221539 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3  
284261 0.6398576 uncharacterized hematopoietic stem/progenitor cells protein MDS030  
236034 0.8541082 uncoupling protein 2 (mitochondrial, proton carrier)  
455269 0.4761389 **Unknown, from Soares 1NFLS-S1**  
769600 0.763743 uracil-DNA glycosylase 2  
2072862 -0.5694163 v-akt murine thymoma viral oncogene homolog 2  
810057 -0.7363941 vasoactive intestinal peptide receptor 1  
855563 0.4941473 v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3  
71087 -0.870641 v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F  
193913 -0.8724313 v-yes-1 Yamaguchi sarcoma viral related oncogene homolog  
784140 0.4984039 WD repeat domain 15  
235986 0.5371486 wingless-type MMTV integration site family, member 11  
138189 0.8950816 Wolfram syndrome 1 (wolframin)  
813281 0.4659334 WW domain-containing protein 1  
795185 0.7765346 xenotropic and polytropic retrovirus receptor  
209537 -0.7245778 zinc finger protein 221

**Table 4** (in alphabetical order)

<b>CloneID</b>	<b>Weight</b>	<b>Description</b>
770785	0.600311	1,2-alpha-mannosidase IC
1574058	0.6796357	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
430614	0.438809	2,3-bisphosphoglycerate mutase
588911	0.3427563	2',5'-oligoadenylate synthetase 1 (40-46 kD)
73252	-0.7283898	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)
838366	0.5072623	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)

489755 -0.5730453 a disintegrin and metalloproteinase domain 12 (meltrin alpha)  
713782 0.6149877 a disintegrin and metalloproteinase domain 15 (metarginidin)  
704254 0.7061648 a disintegrin and metalloproteinase domain 8  
1738208 0.5240868 a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4  
2306682 -0.6934667 A kinase (PRKA) anchor protein (yotiao) 9  
2388571 -0.5459823 A kinase (PRKA) anchor protein 8  
488505 0.4981852 accessory proteins BAP31/BAP29  
809894 -0.491862 acetyl-CoA synthetase  
1587863 0.3980812 acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)  
825013 -0.505654 acidic protein rich in leucines  
823930 0.4800704 actin related protein 2/3 complex, subunit 1A (41 kD)  
1473922 0.6450042 actin related protein 2/3 complex, subunit 3 (21 kD)  
340558 0.6550804 actin related protein 2/3 complex, subunit 5 (16 kD)  
726582 -0.6807781 actin-related protein 3-beta  
26617 0.3371923 activated leucocyte cell adhesion molecule  
265592 0.4615543 activated RNA polymerase II transcription cofactor 4  
51448 -0.5031992 activating transcription factor 3  
2549634 0.3692338 activator of S phase kinase  
768377 0.3809674 activity-dependent neuroprotective protein  
810358 -0.5403705 acyl-Coenzyme A dehydrogenase, very long chain  
210862 0.4683996 acyl-Coenzyme A oxidase 1, palmitoyl  
85450 0.3868399 acyl-Coenzyme A oxidase 2, branched chain  
343607 0.5588222 AD-015 protein  
323693 0.5047237 adaptor-related protein complex 1, sigma 1 subunit  
788641 0.3638059 adaptor-related protein complex 1, sigma 2 subunit  
739109 0.4986821 adaptor-related protein complex 2, sigma 1 subunit  
796757 0.5122331 adaptor-related protein complex 3, sigma 1 subunit  
279970 0.5502099 adenosine A2a receptor  
842939 -0.5172329 adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)  
39600 -0.6540275 adenylate kinase 5

878815 0.3478601 ADP-ribosylation factor 3  
51532 0.5758765 ADP-ribosylation factor-like 6 interacting protein

712139 -1.2738321 ADP-ribosylation factor-like 7  
46248 0.640944 ADP-ribosyltransferase (NAD<sup>+</sup>; poly (ADP-ribose) polymerase)

241489 -0.6212938 adrenergic, beta-2-, receptor, surface  
774446 0.5181672 adrenomedullin  
823851 -0.6182341 AE-binding protein 1  
2095066 -0.676021 alcohol dehydrogenase 1C (class I), gamma polypeptide

814798 -0.9559895 aldehyde dehydrogenase 1 family, member A3  
47853 0.445149 aldehyde dehydrogenase 4 family, member A1

812105 0.3731726 ALL1-fused gene from chromosome 1q  
272706 -0.5914377 alpha2,3-sialyltransferase  
1584628 -0.6102937 alpha-actinin-2-associated LIM protein  
1635320 -0.9586226 amiloride-sensitive cation channel 2, neuronal

1605178 0.3416196 amino acid transporter system A1  
248631 -0.9106505 aminomethyltransferase (glycine cleavage system protein T)

809998 -0.5144681 amylase, alpha 2A; pancreatic  
809998 -0.5297152 **amylase, alpha 2A; pancreatic**  
184022 -0.7070266 amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)  
2250839 0.4266248 androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)

502753 -0.5724623 angiopoietin 2  
505289 0.3595549 angiotensin II, type I receptor-associated protein

128711 0.3437491 anillin (*Drosophila* Scraps homolog), actin binding protein

208718 -0.9190244 annexin A1  
666879 -1.0463245 annexin A8  
239568 0.767277 annexin A9  
1435862 0.7697423 antigen identified by monoclonal antibodies 12E7, F21 and O13

755881 -0.5473964 aquaporin 5  
1568825 0.4829928 Arg/Abl-interacting protein ArgBP2  
767487 0.3530592 ariadne (*Drosophila*) homolog, ubiquitin-conjugating enzyme E2-binding protein, 1  
824799 -0.6054867 ART-4 protein  
2110511 0.5987863 artemin

50519 -0.5577761 aryl hydrocarbon receptor nuclear translocator-like  
183440 0.3406314 arylsulfatase A  
703707 0.4599434 aspartate beta-hydroxylase  
281476 0.3210873 aspartylglucosaminidase  
377275 -1.3102234 ataxia-telangiectasia group D-associated protein  
712023 -0.5302372 AT-binding transcription factor 1  
782439 0.3413092 ATP synthase, H<sup>+</sup> transporting, mitochondrial F0 complex, subunit e  
815737 -0.8444322 ATP synthase, H<sup>+</sup> transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle  
825386 0.4121622 ATP synthase, H<sup>+</sup> transporting, mitochondrial F1F0, subunit d  
2018821 0.5887114 ATPase inhibitor precursor  
754625 0.3503938 ATPase, Class II, type 9A  
266312 0.3289707 ATPase, Cu<sup>++</sup> transporting, beta polypeptide (Wilson disease)  
810725 0.7115051 ATPase, H<sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD  
48518 -0.4966991 ATP-binding cassette, sub-family A (ABC1), member 5  
813256 -0.7731864 ATP-binding cassette, sub-family B (MDR/TAP), member 1  
767798 0.560181 ATX1 (antioxidant protein 1, yeast) homolog 1  
753897 0.4324066 autocrine motility factor receptor  
244764 0.5450377 B7 homolog 3  
796694 0.6893307 baculoviral IAP repeat-containing 5 (survivin)  
1709791 0.7837549 BAI1-associated protein 1  
1609665 -0.8086161 BarH-like homeobox 2  
302549 0.3340582 basic transcription element binding protein 1  
1898758 -0.6126872 BCE-1 protein  
810552 -0.5768989 B-cell associated protein  
1456701 0.6038789 B-cell CLL/lymphoma 9  
1565079 0.358728 B-cell linker  
2244196 0.5972111 B-cell receptor-associated protein BAP29  
814899 0.4840969 BCL2/adenovirus E1B 19kD-interacting protein 3-like  
2043167 0.7167431 BCL2-associated athanogene 3  
1916575 0.3814206 BCL2-interacting killer (apoptosis-inducing)  
1568561 0.3518952 BCL2-like 1  
809357 0.5767382 Bernardinelli-Seip congenital lipodystrophy 2 (seipin)

786069 -0.9203158 beta-site APP-cleaving enzyme  
741977 0.7538359 B-factor, properdin  
1420370 0.6344209 biliverdin reductase B (flavin reductase (NADPH))  
  
1733262 0.4289711 BLu protein  
811024 0.5646461 bone marrow stromal cell antigen 2  
41208 -0.865227 bone morphogenetic protein 1  
1616253 0.567837 breast carcinoma amplified sequence 1  
191904 0.5770884 BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog  
781047 0.357207 budding uninhibited by benzimidazoles 1 (yeast homolog)  
  
588436 0.3544892 butyrate-induced transcript 1  
271472 0.6978431 C3HC4-like zinc finger protein  
1601845 -0.5074894 Ca<sup>2+</sup>-promoted Ras inactivator  
754653 0.4405873 cadherin, EGF LAG seven-pass G-type receptor 3, flamingo (Drosophila) homolog  
841679 0.7666686 calcium and integrin binding protein (DNA-dependent protein kinase interacting protein)  
  
49630 0.3858335 calcium channel, voltage-dependent, L type, alpha 1D subunit  
  
346134 0.4209894 calcium-regulated heat-stable protein (24kD)  
  
772913 -0.8306579 calreticulin  
144881 0.3461767 calumenin  
789383 0.3341667 cAMP responsive element modulator  
839796 -0.6807912 candidate tumor suppressor p33 ING1 homolog  
  
785793 0.4367093 capping protein (actin filament) muscle Z-line, alpha 1  
53039 0.3659853 carbohydrate (keratan sulfate Gal-6) sulfotransferase 1  
  
1660666 0.332029 carbonic anhydrase VB, mitochondrial  
649084 0.4275738 carbonic anhydrase XI  
1412245 0.3762847 carboxypeptidase A2 (pancreatic)  
67765 0.6300886 carboxypeptidase M  
753301 -0.5171758 carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)  
509823 0.7304507 carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)  
  
744417 0.7356767 carnitine acetyltransferase  
122091 0.3903482 casein kinase 2, alpha 1 polypeptide  
377314 -0.561312 casein kinase 2, alpha prime polypeptide  
120106 -0.5770131 caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)

30170 0.3782337 caspase 3, apoptosis-related cysteine protease  
341763 -0.4953701 caspase 5, apoptosis-related cysteine protease  
72778 -1.1752838 caspase 7, apoptosis-related cysteine protease  
1878409 -0.7869766 catechol-O-methyltransferase  
774754 -0.6243946 catenin (cadherin-associated protein), beta 1 (88kD)  
51083 0.5162686 catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)  
345538 0.4875796 cathepsin L  
842994 0.6343858 cathepsin Z  
377461 -1.2798035 caveolin 1, caveolae protein, 22kD  
1946448 -0.7150027 caveolin 2  
1572298 -0.6228686 CD3Z antigen, zeta polypeptide (TiT3 complex)  
208001 -0.5640857 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)  
725454 0.6669973 CDC28 protein kinase 2  
683059 -0.6216483 Cdc42 effector protein 3  
854645 -0.5723062 CDC-like kinase 3  
786067 0.390151 cell division cycle 25B  
415102 0.4387892 cell division cycle 25C  
376516 0.5195127 cell division cycle 4-like  
78869 0.3954821 cell membrane glycoprotein, 110000M(r) (surface antigen)  
739193 -0.5457998 cellular retinoic acid-binding protein 1  
2017415 0.43546 centromere protein A (17kD)  
366067 0.625758 cerebellar degeneration-related protein (62kD)  
1626996 -0.682449 c-fos induced growth factor (vascular endothelial growth factor D)  
429222 0.3239231 CGI-107 protein  
2108077 0.6312583 CGI-112 protein  
726439 0.4067151 CGI-143 protein  
1947647 0.4887766 CGI-147 protein  
753400 0.5732322 CGI-204 protein  
811774 0.9073627 CGI-49 protein  
79032 0.3816428 CGI-82 protein  
624667 0.5828923 CGI-92 protein  
884425 0.5327862 chaperonin containing TCP1, subunit 5 (epsilon)  
882484 0.5165756 chaperonin containing TCP1, subunit 7 (eta)  
221846 -0.6982802 checkpoint suppressor 1

283023 -0.8413949 chemokine (C-X3-C) receptor 1  
429387 0.3810004 chimerin (chimaerin) 2  
770212 -0.4981295 chitinase 3-like 1 (cartilage glycoprotein-39)  
  
72050 0.4114235 chloride channel, nucleotide-sensitive, 1A  
302996 0.3698028 chloride intracellular channel 3  
24729 -0.5302207 cholinergic receptor, muscarinic 1  
2783721 -0.6854649 cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)  
  
2094232 0.3693257 chromosome 1 open reading frame 12  
293569 0.5103638 chromosome 1 open reading frame 21  
742562 -0.730047 chromosome 16 open reading frame 5  
1492426 0.8445255 chromosome 19 open reading frame 3  
824052 0.6375787 chromosome 6 open reading frame 1  
469383 0.5558732 chromosome 8 open reading frame 1  
811149 -0.9216006 chromosome 9 open reading frame 3  
731308 0.5371204 citrate synthase  
1634832 -0.5931096 class I cytokine receptor  
124331 0.5025464 cleavage and polyadenylation specific factor 5, 25 kD subunit  
  
815026 0.4472842 cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD  
  
510794 0.4264564 c-myc binding protein  
1656062 0.4355127 coagulation factor XII (Hageman factor)  
769959 -0.6720196 collagen, type IV, alpha 2  
263716 -0.6767498 collagen, type VI, alpha 1  
488258 -0.7574184 collagen, type XVI, alpha 1  
1632252 0.404193 complement component 1, q subcomponent, alpha polypeptide  
  
85634 -0.4961026 complement component 1, s subcomponent  
  
77972 -0.7194713 complement component 3  
898092 -0.7267434 connective tissue growth factor  
230910 -0.6096107 **contig C004028, human**  
1519147 -0.7548183 **contig C028965, human**  
127646 0.4493747 **contig C030249, human**  
823909 0.3675927 **contig C039966, human**  
177665 -0.6624986 **contig C055081, human**  
770992 0.3331315 **contig C056172, human**  
897770 0.4270685 **contig C071196, human**  
504940 -0.508056 **contig C075945, human**  
108425 0.6008772 **contig C076797, human**  
155806 0.3741516 **contigs C041196 and C066478, human**  
119290 -0.8224756 cortic al thymocyte receptor (X. laevis CTX) like  
  
283751 0.4567022 cortistatin

489823 0.4468978 COX17 (yeast) homolog, cytochrome c oxidase assembly protein  
1416782 0.4558415 creatine kinase, brain  
839736 -1.2271618 crystallin, alpha B  
1555924 -0.8025163 CSR1 protein  
488956 -0.70192 CUG triplet repeat, RNA-binding protein 2  
701751 0.561139 cut (*Drosophila*)-like 1 (CCAAT displacement protein)  
  
487444 0.3357395 cyclic AMP phosphoprotein, 19 kD  
2308346 -0.5268833 cyclin-dependent kinase 2  
742595 0.6265846 cyclin-dependent kinase 5  
757873 -0.6940266 cyclin-dependent kinase 5, regulatory subunit 1 (p35)  
  
700792 0.4949149 cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)  
1323448 1.397391 cysteine-rich protein 1 (intestinal)  
360254 -0.9286811 cysteine-rich, angiogenic inducer, 61  
796984 -0.5010588 cytochrome b-245, beta polypeptide (chronic granulomatous disease)  
196189 0.5916252 cytochrome b-5  
1455394 0.3811391 cytochrome c  
278531 0.4663008 cytochrome c oxidase subunit VIc  
1601947 0.6045149 cytochrome c oxidase subunit VIIa polypeptide 2 (liver)  
  
884511 0.3440809 cytochrome c oxidase subunit VIIb  
38356 0.4513099 cytochrome P450, subfamily 46 (cholesterol 24-hydroxylase)  
  
768064 0.673441 cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1  
724888 0.3272422 cytochrome P450, subfamily IVB, polypeptide 1  
  
162775 -0.5385174 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)  
2018423 -0.501705 death-associated protein kinase 2  
810039 0.3662086 defender against cell death 1  
296702 0.4670993 deiodinase, iodothyronine, type I  
1492468 0.4878466 DEME-6 protein  
810156 0.4561539 deoxythymidylate kinase (thymidylate kinase)  
  
1161564 -1.3891189 desmuslin  
842980 0.6081528 developmentally regulated GTP-binding protein 1  
  
415613 -0.5528761 DHHC1 protein  
795401 0.3573481 diacylglycerol O-acyltransferase (mouse) homolog  
  
813387 0.4727653 diaphorase (NADH/NADPH) (cytochrome b-5 reductase)

760299 -1.7010462 dickkopf (*Xenopus laevis*) homolog 3  
35828 -0.7163689 diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)  
742685 -1.272916 disabled (*Drosophila*) homolog 2 (mitogen-responsive phosphoprotein)  
767761 0.4608709 DKFZP434B168 protein  
810998 0.3179036 DKFZP434C131 protein  
825740 0.5762093 DKFZp434J1813 protein  
366353 0.6203012 DKFZP564C186 protein  
770766 0.4603527 DKFZP564C1940 protein  
593840 -0.5033966 DKFZP564K1964 protein  
345423 0.4694596 DKFZP564M112 protein  
1635062 -0.8243024 DKFZP586A011 protein  
294397 0.3744208 DKFZP586A0522 protein  
2011515 0.5566484 DKFZP586B0923 protein  
825282 0.3624112 DKFZP586L0724 protein  
1909433 -0.5638242 DKFZP727C091 protein  
202514 0.5045411 DNA (cytosine-5-)-methyltransferase 3 alpha  
  
276915 0.3851081 DNA (cytosine-5-)-methyltransferase 3 beta  
  
809466 0.3568464 DNA segment on chromosome 19 (unique) 1177 expressed sequence  
754046 0.3464097 DNA segment on chromosome X (unique) 9879 expressed sequence  
263727 0.4767486 DNA segment, single copy probe LNS-CAI/LNS-CAII (deleted in polyposis)  
454896 0.5013449 DnaJ (Hsp40) homolog, subfamily A, member 2  
  
1637302 0.3353374 DNAJ domain-containing  
2018527 0.4717524 dolichyl-phosphate mannosyltransferase polypeptide 3  
  
884462 -0.8743987 Down syndrome critical region gene 1  
154610 0.4410751 dynactin 4  
593023 -0.7516846 dystrobrevin, beta  
1864302 -0.6932327 E74-like factor 5 (ets domain transcription factor)  
  
840944 -0.7099353 early growth response 1  
781017 -0.8526926 early growth response 2 (*Krox-20* (*Drosophila*) homolog)  
  
431231 -0.7182897 EGF-containing fibulin-like extracellular matrix protein 2  
188335 -0.7399294 egf-like module containing, mucin-like, hormone receptor-like sequence 2  
295986 0.413087 emopamil-binding protein (sterol isomerase)

2248488 0.4645687 ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate))  
823574 0.457224 endosulfine alpha  
66532 -0.5773248 endothelin 3  
122147 0.5067128 **engulfment and cell motility 2 (ced-12 homolog, C. elegans) (ELMO2), Homo sapiens**  
2252954 -0.6687686 enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related)  
366834 0.3217743 envoplakin  
153760 -0.9227865 EphB1  
813520 -0.7092422 EphB3  
1474684 0.3291536 ephrin-A1  
811088 -1.0851546 ephrin-B3  
1577736 -0.6215965 epidermal growth factor (beta-urogastrone)  
109863 0.559767 epithelial membrane protein 2  
785967 -0.6049171 erythrocyte membrane protein band 4.1-like 2  
  
34093 -0.8800259 EST  
208969 -0.561267 EST  
594500 0.5474088 EST  
1623016 -0.6263561 EST  
1641894 0.4277815 EST  
358267 0.4719017 EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]  
  
415415 -0.646492 EST, Moderately similar to RL1X\_HUMAN 60S RIBOSOMAL PROTEIN L18A [H.sapiens]  
  
27769 -0.8298821 ESTs  
34150 -0.7263513 ESTs  
40027 -0.7779473 ESTs  
41826 0.4456463 ESTs  
43679 -0.5063146 ESTs  
46716 0.3557556 ESTs  
53081 -0.5446617 ESTs  
70606 0.481356 ESTs  
75078 -0.6362307 ESTs  
81316 -0.6176265 ESTs  
83358 0.4380365 ESTs  
134192 -0.4908497 ESTs  
134918 0.3779855 ESTs  
139660 -0.7677153 ESTs  
140635 0.4706227 ESTs  
160609 -0.8405669 ESTs  
162308 -0.7654139 **ESTs**  
162308 -0.8910356 ESTs  
196435 -0.9665947 ESTs

197056 -0.5128128 ESTs  
214996 0.380548 ESTs  
250313 0.4121296 ESTs  
266500 0.3758559 ESTs  
281190 -0.7927001 ESTs  
290101 0.4071477 ESTs  
298143 0.3307258 ESTs  
300099 0.3547857 ESTs  
344091 0.4871044 ESTs  
365738 0.6740773 ESTs  
415816 -0.8887425 ESTs  
462939 -0.5662456 ESTs  
470148 -0.712917 ESTs  
544639 -0.8275232 ESTs  
564847 0.573202 ESTs  
564981 0.4782207 ESTs  
725622 -0.5370309 ESTs  
754628 0.7195265 ESTs  
757191 -0.8247438 ESTs  
782547 0.3708058 ESTs  
784105 0.5259815 ESTs  
812161 -0.4948424 ESTs  
814209 0.4602081 ESTs  
814826 -0.8443265 ESTs  
827171 0.7154964 ESTs  
839580 0.3216628 ESTs  
1027283 0.3242547 ESTs  
1257131 -0.8163443 ESTs  
1466893 -0.6364598 ESTs  
1500162 0.6416738 ESTs  
1517749 0.5045134 ESTs  
1522734 -0.5618289 ESTs  
1534493 -0.5376323 ESTs  
1536006 0.5590182 ESTs  
1537001 0.59528 ESTs  
1557637 0.3805285 ESTs  
1558233 0.4622449 ESTs  
1577920 -0.5496944 ESTs  
1585492 0.3812472 ESTs  
1637829 0.3246232 ESTs  
1700436 0.5569949 ESTs  
1707637 -0.5964339 ESTs  
1712825 -0.6204409 ESTs  
1899312 0.3551595 ESTs  
1909935 -0.8169271 ESTs

1911663 -0.5168962 ESTs  
2046679 0.3358043 ESTs  
431505 0.5670119 ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]  
279633 0.3907503 ESTs, Highly similar to I38759 zinc finger/leucine zipper protein [H.sapiens]  
289760 -1.1390686 ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]  
345023 -0.5166203 ESTs, Highly similar to T08701 hypothetical protein DKFZp564N123.1 [H.sapiens]  
322024 -0.5714933 ESTs, Highly similar to T12495 hypothetical protein DKFZp434H071.1 [H.sapiens]  
46129 -0.6919169 ESTs, Highly similar to T17245 hypothetical protein DKFZp586J0917.1 [H.sapiens]  
79726 0.4162264 ESTs, Highly similar to T46395 hypothetical protein DKFZp434I1120.1 [H.sapiens]  
279720 0.3282308 ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]  
725978 0.5147267 ESTs, Moderately similar to ALU7\_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]  
530197 0.6122721 ESTs, Moderately similar to ALU8\_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]  
593431 0.5235073 ESTs, Moderately similar to CEGT\_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]  
345670 -1.4445337 ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]  
529843 -1.0036824 ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]  
120749 0.5060444 ESTs, Moderately similar to KIAA1215 protein [H.sapiens]  
283124 -0.7933772 ESTs, Moderately similar to LONG-CHAIN FATTY ACID TRANSPORT PROTEIN [M.musculus]  
138242 -0.5621088 ESTs, Moderately similar to MAS2\_HUMAN MANNAN-BINDING LECTIN SERINE PROTEASE 2 PRECURSOR [H.sapiens]

289505 0.3714361 ESTs, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]

179212 0.3649976 ESTs, Moderately similar to T12539 hypothetical protein DKFZp434J154.1 [H.sapiens]

1926246 -0.701769 ESTs, Moderately similar to T46371 hypothetical protein DKFZp434P1018.1 [H.sapiens]

160192 -1.1751869 ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]

2017721 0.3781067 ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]

810497 0.3367408 ESTs, Weakly similar to A35363 synapsin I splice form a [H.sapiens]

73009 0.4822587 ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]

726699 0.3695061 ESTs, Weakly similar to AAB47496 NG5 [H.sapiens]

746163 0.5009715 ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

770848 -0.5767154 ESTs, Weakly similar to ALU1\_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

346902 -0.5794362 ESTs, Weakly similar to ALU2\_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]

2016908 0.8282806 ESTs, Weakly similar to CA13\_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]

488642 0.4881613 ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]

128695 0.3455381 ESTs, Weakly similar to I38344 titin, cardiac muscle [H.sapiens]

1640821 0.7790286 ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]

841621 0.4020253 ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

742707 0.6476434 ESTs, Weakly similar to MUC2\_HUMAN MUCIN 2 PRECURSOR [H.sapiens]

767164 -0.842198 ESTs, Weakly similar to MUC2\_HUMAN MUCIN 2 PRECURSOR [H.sapiens]

2029173 0.8213721 ESTs, Weakly similar to N-WASP [H.sapiens]

753745 -0.4917192 ESTs, Weakly similar to S57447 HPBRII-7 protein [H.sapiens]  
1583198 0.39981 ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]  
1897944 -0.4855156 ESTs, Weakly similar to T00366 hypothetical protein KIAA0669 [H.sapiens]  
2572170 0.4277651 ESTs, Weakly similar to T26581 hypothetical protein Y32B12A.3 - Caenorhabditis elegans [C.elegans]  
358936 0.4314082 ESTs, Weakly similar to T2D3\_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]  
743589 0.568516 ESTs, Weakly similar to T2D3\_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]  
35147 1.0886084 ESTs, Weakly similar to unnamed protein product [H.sapiens]  
1910078 0.3491481 ESTs, Weakly similar to YK54\_YEAST HYPOTHETICAL 18.4 KD PROTEIN IN SIS2-MTD1 INTERGENIC REGION [S.cerevisiae]  
488202 0.8463961 ESTs, Weakly similar to YZ28\_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]  
414999 -0.5002542 ets variant gene 4 (E1A enhancer-binding protein, E1AF)  
796542 -1.2625621 ets variant gene 5 (ets-related molecule)  
1590021 -0.5302114 ets variant gene 6 (TEL oncogene)  
299720 -0.5284407 **eukaryotic translation elongation factor 1 alpha 1**  
299720 -0.5378801 eukaryotic translation elongation factor 1 alpha 1  
299720 -0.5388238 eukaryotic translation elongation factor 1 alpha 1  
299720 -0.5565137 **eukaryotic translation elongation factor 1 alpha 1**  
811837 -0.848137 **eukaryotic translation elongation factor 1 alpha 1**  
811837 -0.8764231 eukaryotic translation elongation factor 1 alpha 1  
469151 0.4462659 eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD )  
824479 0.3225263 exonuclease NEF-sp  
74566 0.3226444 exportin 1 (CRM1, yeast, homolog)  
301122 0.5368073 extracellular matrix protein 1  
741139 -0.8299902 eyes absent (Drosophila) homolog 2  
782503 0.4334388 fatty acid desaturase 1  
1758590 0.6040962 fatty-acid-Coenzyme A ligase, long-chain 3  
858167 -0.6453859 fatty-acid-Coenzyme A ligase, long-chain 4  
1469148 0.3776558 FGFR1 oncogene partner

855755 -0.4897236 fibrillarin  
154472 -0.6253276 fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)  
  
752631 0.650399 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)  
789012 0.6104002 fibulin 2  
1570663 0.3656056 FK506-binding protein 4 (59kD)  
813616 0.3608471 FK506-binding protein like  
376875 0.490328 flavin containing monooxygenase 1  
131839 -1.2372478 folate receptor 1 (adult)  
772220 0.4352917 for protein disulfide isomerase-related  
628955 -0.8761473 forkhead box O1A (rhabdomyosarcoma)  
796475 -0.8041136 four and a half LIM domains 3  
52419 -1.0368509 Friedreich ataxia region gene X123  
298134 -0.6152731 frizzled (Drosophila) homolog 1  
2309073 0.5226599 frizzled (Drosophila) homolog 5  
298122 -1.1962478 frizzled (Drosophila) homolog 7  
140071 -0.5708303 frizzled-related protein  
1499828 0.4030396 fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)  
  
183200 0.4697062 fumarylacetoacetate hydrolase (fumarylacetoacetase)  
204686 0.4687565 FXYD domain-containing ion transport regulator 1 (phospholemman)  
2016775 -0.8063264 G protein-coupled receptor, family C, group 5, member B  
  
842825 0.5047729 G1 to S phase transition 1  
81409 -0.6338327 GABA(A) receptor-associated protein like 1  
  
469306 -0.5113377 gastrin-releasing peptide  
214068 0.3414185 GATA-binding protein 3  
1393018 0.5404243 general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD )  
2016194 0.4417536 glia maturation factor, beta  
1708055 0.3225042 glioblastoma overexpressed  
741474 0.7732047 glucose phosphate isomerase  
2018337 0.4833207 glucosidase, beta; acid (includes glucosylceramidase)  
  
1609836 1.0164283 glutamate-ammonia ligase (glutamine synthase)  
868400 -0.4928479 glutaminyl-tRNA synthetase  
731044 0.8169506 glutaredoxin 2  
1848977 0.5015371 glycerol kinase  
344720 -1.5196431 glycophorin C (Gerbich blood group)  
491001 0.3884144 glyoxalase I

358217 0.4385343 glycan 4  
686552 0.7231319 golgi phosphoprotein 1  
811582 0.3319191 golgi phosphoprotein 2  
431805 0.405447 granulin  
323238 -0.7042807 GRO1 oncogene (melanoma growth stimulating activity, alpha)  
  
1556433 -1.1222978 GRO3 oncogene  
752643 0.5732323 group XII secreted phospholipase A2  
796181 -0.8888496 growth arrest-specific 6  
131268 0.3564734 growth factor receptor-bound protein 14  
788654 0.6866898 **growth factor receptor-bound protein 2**  
788654 1.2615322 growth factor receptor-bound protein 2  
810063 0.620086 growth factor, erv1 (*S. cerevisiae*)-like (augmenter of liver regeneration)  
51741 0.4678807 GTP-binding protein  
767765 -0.7691523 GTP-binding protein overexpressed in skeletal muscle  
  
308466 0.6800103 GTP-binding protein Sara  
292213 0.4014458 guanine nucleotide binding protein (G protein), beta polypeptide 2  
190059 -0.634814 guanine nucleotide binding protein (G protein), gamma 7  
  
1032831 -0.5764161 glycosyltransferase  
1711456 -0.4896574 H factor (complement)-like 1  
66317 0.4132405 H1 histone family, member 2  
283919 0.937383 H2A histone family, member L  
488964 0.9569176 H2A histone family, member O  
290841 0.8346933 H2B histone family, member A  
1500000 1.0118809 H2B histone family, member B  
430235 0.5874504 H2B histone family, member Q  
815781 0.4441245 heat shock 105kD  
1870305 -0.6958213 heat shock 27kD protein 2  
471568 0.8264546 hematological and neurological expressed 1  
  
1569187 -1.2971252 heparan sulfate (glucosamine) 3-O-sulfotransferase 4  
  
1486082 -0.6635259 heparin-binding growth factor binding protein  
  
770845 0.5870877 hexokinase 1  
1637282 0.4777562 hexokinase 2  
345787 0.4647372 highly expressed in cancer, rich in leucine heptad repeats  
  
172517 0.5869599 hippocalcin-like 1  
2116188 -0.5046972 histone deacetylase 5  
1434948 0.3849593 HIV TAT specific factor 1  
325365 -0.7012106 HIV-1 rev binding protein 2  
611481 -0.6894079 HMG-box transcription factor TCF-3

1434905 0.3624537 homeo box B7  
347726 0.377767 homeo box D8  
1592715 0.4944665 Homer, neuronal immediate early gene, 3  
669379 0.4011648 Homo sapiens BAC clone RP11-505D17 from 7p22-p21  
486179 -0.5443525 Homo sapiens cDNA FLJ10205 fis, clone HEMBA1004954  
742581 0.440367 Homo sapiens cDNA FLJ10366 fis, clone NT2RM2001420  
323780 -0.8879854 Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402  
796152 -0.6356106 Homo sapiens cDNA FLJ11685 fis, clone HEMBA1004934  
825356 -0.533771 Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458  
1474424 0.5021308 Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328  
308539 -0.6726187 Homo sapiens cDNA FLJ12777 fis, clone NT2RP2001720  
566443 0.3705134 Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033  
212542 0.5587394 Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321  
270826 -0.9389651 Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795  
681992 -0.7691299 Homo sapiens cDNA FLJ13384 fis, clone PLACE1001062,  
highly similar to Homo sapiens mRNA for lysine-ketoglutarate  
reductase/saccharopine dehydrogenase  
647866 0.3706822 Homo sapiens cDNA FLJ13975 fis, clone Y79AA1001585  
283739 0.3714571 Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838  
366156 0.3861394 Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838  
487831 0.3464379 Homo sapiens cDNA FLJ14059 fis, clone HEMBB1000573  
825327 0.6094796 Homo sapiens cDNA FLJ14105 fis, clone MAMMA1001202  
35626 0.39822 Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955  
503671 -0.5461871 Homo sapiens cDNA FLJ14368 fis, clone HEMBA1001122  
594226 0.403676 Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409  
1492780 0.6544659 Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409  
488130 -0.5289721 Homo sapiens cDNA FLJ20767 fis, clone COL06986

823615 0.3462131 Homo sapiens cDNA: FLJ21245 fis, clone COL01184  
770675 0.454729 Homo sapiens cDNA: FLJ21323 fis, clone COL02374  
564801 -0.5824549 Homo sapiens cDNA: FLJ21409 fis, clone COL03924  
131094 0.8675719 Homo sapiens cDNA: FLJ21587 fis, clone COL06946  
810097 -0.5487174 Homo sapiens cDNA: FLJ21721 fis, clone COLF0381  
220293 -0.5078291 Homo sapiens cDNA: FLJ21800 fis, clone HEP00618  
1500815 -0.4934665 Homo sapiens cDNA: FLJ22130 fis, clone HEP19632  
814528 0.6878182 Homo sapiens cDNA: FLJ22139 fis, clone HEP20959  
68534 -0.5724394 Homo sapiens cDNA: FLJ22290 fis, clone HRC04405  
753071 -1.2529315 Homo sapiens cDNA: FLJ22528 fis, clone HRC12825  
840266 -1.1476896 Homo sapiens cDNA: FLJ22667 fis, clone HSI08385  
491186 -0.5507413 Homo sapiens cDNA: FLJ23131 fis, clone LNG08502  
745394 0.4147627 Homo sapiens cDNA: FLJ23249 fis, clone COL04196  
2017917 0.360911 Homo sapiens cDNA: FLJ23371 fis, clone HEP16068, highly similar to HSTFIISH Homo sapiens mRNA for transcription elongation factor TFIIS  
727078 0.6263882 Homo sapiens cDNA: FLJ23602 fis, clone LNG15735  
823694 0.4280476 Homo sapiens chromosome 19, BAC CIT-HSPC\_204F22 (BC228680), complete sequence; contains bacterial insertion element  
491519 -0.561401 Homo sapiens clone 24775 mRNA sequence  
78736 0.3354693 Homo sapiens clone 24877 mRNA sequence  
649977 0.3534567 Homo sapiens clone CDABP0014 mRNA sequence  
796723 0.8573155 Homo sapiens clone CDABP0014 mRNA sequence  
502689 -0.6739476 Homo sapiens clone HH409 unknown mRNA  
415589 0.3296266 Homo sapiens clone PP1498 unknown mRNA  
855406 0.3241172 Homo sapiens clone TCCCIA00176 mRNA sequence

488404 -0.9880176 Homo sapiens clone TUA8 Cri-du-chat region mRNA  
768452 0.6018854 Homo sapiens EST from clone 491476, full insert  
752837 -0.5794612 Homo sapiens mRNA for FLJ00074 protein, partial cds  
2028916 0.3516982 Homo sapiens mRNA for Hmob33 protein, 3' untranslated region  
282404 -0.5528532 Homo sapiens mRNA for KIAA1671 protein, partial cds  
743977 0.4368155 Homo sapiens mRNA for TL132  
1968422 -0.5802058 Homo sapiens mRNA full length insert cDNA clone  
EUROIMAGE 1968422  
327506 0.4152106 Homo sapiens mRNA full length insert cDNA clone  
EUROIMAGE 327506  
70245 -0.795375 Homo sapiens mRNA full length insert cDNA clone  
EUROIMAGE 50374  
970590 -0.8333968 Homo sapiens mRNA; cDNA DKFZp434A115 (from clone  
DKFZp434A115)  
119133 0.3564449 Homo sapiens mRNA; cDNA DKFZp434B231 (from clone  
DKFZp434B231)  
44292 0.6122043 Homo sapiens mRNA; cDNA DKFZp434C107 (from clone  
DKFZp434C107)  
1871116 -0.9821709 Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone  
DKFZp434C1714); partial cds  
24958 -0.7225195 Homo sapiens mRNA; cDNA DKFZp434C2016 (from clone  
DKFZp434C2016)  
1883028 0.3345488 Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone  
DKFZp434J1912)  
754157 -0.7165332 Homo sapiens mRNA; cDNA DKFZp434K2172 (from clone  
DKFZp434K2172)  
2016648 0.7633048 Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone  
DKFZp434N1728)  
785538 -0.6289951 Homo sapiens mRNA; cDNA DKFZp434N2116 (from clone  
DKFZp434N2116)  
265103 0.5361177 Homo sapiens mRNA; cDNA DKFZp547M123 (from clone  
DKFZp547M123)  
565319 1.0969429 Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone  
DKFZp564B1264)

813265 -1.2230435 Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)  
486683 -1.2614406 Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)  
1844765 0.57783 Homo sapiens mRNA; cDNA DKFZp564O1763 (from clone DKFZp564O1763)  
67067 -0.6003961 Homo sapiens mRNA; cDNA DKFZp564O222 (from clone DKFZp564O222)  
490668 -0.7364434 Homo sapiens mRNA; cDNA DKFZp586B211 (from clone DKFZp586B211)  
754192 0.3225824 Homo sapiens mRNA; cDNA DKFZp586H0924 (from clone DKFZp586H0924)  
1461477 0.5343834 Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)  
1584540 -0.9754693 Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)  
595637 -0.5373697 Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012)  
132857 -1.0084069 Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)  
744918 -0.6552361 Homo sapiens mRNA; cDNA DKFZp761I0911 (from clone DKFZp761I0911)  
22917 -1.1590598 Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)  
343079 -0.5224833 Homo sapiens mRNA; cDNA DKFZp761P0114 (from clone DKFZp761P0114)  
78946 -0.648366 Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence  
74738 0.409593 Homo sapiens, clone IMAGE:3535294, mRNA, partial cds  
1519013 0.3628651 Homo sapiens, clone IMAGE:3537447, mRNA, partial cds  
1631735 0.5502891 Homo sapiens, clone IMAGE:3604336, mRNA, partial cds  
186768 0.6550741 Homo sapiens, clone IMAGE:3604869, mRNA

292770 0.6231261 Homo sapiens, clone IMAGE:3627860, mRNA, partial cds  
767982 -0.533231 Homo sapiens, clone IMAGE:4134852, mRNA, partial cds  
183704 -0.5184644 Homo sapiens, clone MGC:13446 IMAGE:4275731, mRNA, complete cds  
241677 0.3332521 Homo sapiens, clone MGC:18110 IMAGE:4152745, mRNA, complete cds  
1652310 0.4321289 Homo sapiens, clone MGC:19613 IMAGE:3833049, mRNA, complete cds  
810002 -1.3038896 Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds  
810567 0.3243984 Homo sapiens, clone MGC:3182 IMAGE:3356293, mRNA, complete cds  
288748 -0.5493871 Homo sapiens, clone MGC:5352 IMAGE:3048106, mRNA, complete cds  
50892 -0.6887497 Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds  
1635665 0.430087 Homo sapiens, RIKEN cDNA 2010100O12 gene, clone MGC:14813 IMAGE:4133274, mRNA, complete cds  
491527 0.4219324 Homo sapiens, Similar to CG7083 gene product, clone MGC:10534 IMAGE:3957147, mRNA, complete cds  
130835 0.3209345 Homo sapiens, Similar to clone FLB3816, clone IMAGE:3454380, mRNA  
306806 0.324179 Homo sapiens, Similar to hypothetical protein FLJ12838, clone IMAGE:4130879, mRNA, partial cds  
41123 0.3739475 Homo sapiens, Similar to RIKEN cDNA 2210021G21 gene, clone MGC:14859 IMAGE:3621871, mRNA, complete cds  
242706 0.3562469 Homo sapiens, Similar to RIKEN cDNA 5730494N06 gene, clone MGC:13349 IMAGE:4249231, mRNA, complete cds  
839746 0.4699443 Homo sapiens, Similar to RIKEN cDNA 5830420C20 gene, clone IMAGE:3633379, mRNA, partial cds  
1649374 0.3771383 homogentisate 1,2-dioxygenase (homogentisate oxidase)  
1492238 0.9019233 HSPC003 protein  
796469 1.0269115 HSPC150 protein similar to ubiquitin-conjugating enzyme  
772925 0.5562164 HSPCO34 protein  
470099 0.6915952 HT002 protein; hypertension-related calcium-regulated gene  
253884 -0.4897811 Human BAC clone GS1-99H8  
241043 0.3770901 Human clone 137308 mRNA, partial cds

- 83999 -0.5044612 Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to *X. laevis* Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat prote
- 178805 1.0274897 Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to *Drosophila* Scratch (Scrt), Slug and *Xenopus* Snail, a novel gene similar to *Drosophila* CG6762, STSs, GSSs and five CpG
- 277627 -0.5329107 Human SH3 domain-containing protein SH3P18 mRNA, complete cds
- 811585 0.5288102 huntingtin (Huntington disease)
- 1554549 0.9764206 hydroxyacyl glutathione hydrolase
- 813419 0.5447006 hydroxyacyl-Coenzyme A dehydrogenase, type II
- 256619 0.6102239 hydroxysteroid (17-beta) dehydrogenase 7
- 810728 -0.7607171 hypothetical gene ZD52F10
- 80764 0.5510626 hypothetical protein
- 139354 0.4582974 hypothetical protein
- 140289 0.4624364 hypothetical protein
- 595213 0.4824381 hypothetical protein
- 768007 -0.5983563 hypothetical protein
- 785766 0.5731938 hypothetical protein
- 810402 0.5555749 hypothetical protein
- 811848 -1.1350073 hypothetical protein
- 824943 0.3527414 hypothetical protein
- 825822 0.4255725 hypothetical protein
- 841260 0.3801713 hypothetical protein
- 2271240 -0.5782432 hypothetical protein
- 299815 0.4482635 hypothetical protein DC42
- 150118 0.4039789 hypothetical protein DKFZp434F054
- 32489 -0.7571259 hypothetical protein DKFZp566A1524
- 489351 0.7003616 hypothetical protein DKFZp566J2046
- 746190 0.4430243 hypothetical protein DKFZp761B1514
- 76182 -0.9106484 hypothetical protein DKFZp761F241
- 725152 -0.6591675 hypothetical protein DKFZp762A227
- 66406 0.5966701 hypothetical protein DKFZp762E1312
- 842896 -0.5137089 hypothetical protein DKFZp762L0311
- 51657 0.4208387 hypothetical protein ET
- 491465 0.5420241 hypothetical protein FLJ10035
- 767289 0.4323485 hypothetical protein FLJ10055
- 172783 -0.6088873 hypothetical protein FLJ10390

292936	0.4217115	hypothetical protein FLJ10468
753299	0.6694573	hypothetical protein FLJ10504
823907	0.4135955	hypothetical protein FLJ10511
504308	0.5564295	hypothetical protein FLJ10540
131012	-0.4897744	hypothetical protein FLJ10633
503889	0.5930018	hypothetical protein FLJ10656
40042	0.3362557	hypothetical protein FLJ10747
233349	0.5446353	hypothetical protein FLJ10761
246800	0.4927231	hypothetical protein FLJ10803
343695	-0.7706809	hypothetical protein FLJ10875
2052113	0.7627076	hypothetical protein FLJ10903
325515	0.444486	hypothetical protein FLJ10980
41869	-0.6747514	hypothetical protein FLJ11017
126851	0.5454014	hypothetical protein FLJ11160
503335	-0.6944661	hypothetical protein FLJ11196
768570	0.7102463	hypothetical protein FLJ11280
266218	0.4362517	hypothetical protein FLJ11350
589232	0.6551447	hypothetical protein FLJ11506
489594	0.5178551	hypothetical protein FLJ11565
744994	0.3526118	hypothetical protein FLJ12242
743220	0.3566593	hypothetical protein FLJ12517
41569	0.4974126	hypothetical protein FLJ12650
731080	0.4276128	hypothetical protein FLJ12661
84464	-0.5426397	hypothetical protein FLJ12806
785733	-0.6476493	hypothetical protein FLJ12892
785795	0.598504	hypothetical protein FLJ12910
530036	-0.6324794	hypothetical protein FLJ13078
150003	0.8251408	hypothetical protein FLJ13187
810411	0.400096	hypothetical protein FLJ13222
1605426	0.787298	hypothetical protein FLJ13352
770935	-0.8700104	hypothetical protein FLJ13511
248649	0.5975539	hypothetical protein FLJ13910
1554167	-1.0818834	hypothetical protein FLJ14529
1581941	0.5676045	hypothetical protein FLJ14540
1636360	-0.5629882	hypothetical protein FLJ14957
259950	0.364359	hypothetical protein FLJ14991
250797	-0.6124667	hypothetical protein FLJ20038
76196	0.3781541	hypothetical protein FLJ20062
1505038	1.1904802	hypothetical protein FLJ20171
52724	-0.6199204	hypothetical protein FLJ20241
428582	0.4684705	hypothetical protein FLJ20296
2027952	0.3307056	hypothetical protein FLJ20297
753320	0.4744893	hypothetical protein FLJ20533
745490	-0.6329354	hypothetical protein FLJ20607
502774	0.7148695	hypothetical protein FLJ20623

1636092	0.7270017	hypothetical protein FLJ20657
300632	-1.2368481	hypothetical protein FLJ21044 similar to Rbig1
1572710	0.3725734	hypothetical protein FLJ21213
1470278	-0.6633411	hypothetical protein FLJ21841
85804	0.4171445	hypothetical protein FLJ21918
429799	0.6915155	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
1636669	0.4384707	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
811907	0.4340842	hypothetical protein FLJ22056
510575	0.5430211	hypothetical protein FLJ22087
810939	0.40256	hypothetical protein FLJ22169
2015517	0.5742448	hypothetical protein FLJ22237
1493218	-0.884795	hypothetical protein FLJ22297
1947381	0.3509235	hypothetical protein FLJ22329
37554	0.5706008	hypothetical protein FLJ22353
233679	-0.5356625	hypothetical protein FLJ22362
753378	0.548977	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
757328	0.3985331	hypothetical protein FLJ22678
244974	0.4105439	hypothetical protein FLJ22875
52103	0.4988158	hypothetical protein FLJ23045
161998	-0.5044691	hypothetical protein FLJ23138
1417886	-0.4941304	hypothetical protein FLJ23239
220395	-0.6418175	hypothetical protein FLJ23293 similar to ARL-6 interacting protein-2
1632247	0.3312131	hypothetical protein FLJ23436
455275	0.3869874	hypothetical protein FLJ23469
1651906	-0.5863631	hypothetical protein FLJ23544
144880	0.5704416	hypothetical protein from EUROIMAGE 1759349
1696757	0.5254296	hypothetical protein KIAA1165
625693	0.5055986	hypothetical protein MGC10911
131566	0.3261265	hypothetical protein MGC11061
781342	0.4716127	hypothetical protein MGC11115
824879	0.7432221	hypothetical protein MGC11275
773373	-0.6730112	hypothetical protein MGC14258
325606	0.647638	hypothetical protein MGC14353
240752	-0.56913	hypothetical protein MGC14797
1898619	0.4916939	hypothetical protein MGC15737
68636	0.6838604	hypothetical protein MGC2477
743810	0.3667087	hypothetical protein MGC2577
490023	-1.2114805	hypothetical protein MGC2648
815501	0.3214849	hypothetical protein MGC2721
1869201	0.6727191	hypothetical protein MGC2745

1558642	0.4298376	hypothetical protein MGC2771
773487	-0.5686324	hypothetical protein MGC3032
51773	0.6925666	hypothetical protein MGC3077
37708	0.6986007	hypothetical protein MGC3101
814443	-0.8385965	hypothetical protein MGC3232
1570427	-0.5280955	hypothetical protein MGC4309
42408	0.725109	hypothetical protein MGC4604
123614	0.633308	hypothetical protein MGC4675
120271	0.4886584	hypothetical protein MGC4692
120271	0.5982507	hypothetical protein MGC4692
812238	1.0043787	hypothetical protein MGC4692
1858892	0.6904662	hypothetical protein MGC4825
245485	0.3215041	hypothetical protein MGC5178
121251	0.385792	hypothetical protein MGC5576
293727	0.4242722	hypothetical protein MGC861
1597813	-0.5406089	hypothetical protein PP1044
810609	0.4551167	hypothetical protein PP1226
782501	-0.7086066	hypothetical protein PP1665
745606	1.1825585	hypothetical protein PP591
2028949	0.5946445	hypothetical protein PRO1855
701115	0.3936994	hypothetical protein PRO2013
815835	0.3764754	hypothetical protein R33729_1
625399	-0.9066615	hypothetical protein similar to beta-transducin family
238907	-0.5534598	hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142
897806	0.6015789	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
39884	0.7075527	IMP (inosine monophosphate) dehydrogenase 1
1846982	0.3602851	inhibin, beta C
221295	0.5157877	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
788234	-1.3761312	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
505243	-0.6671218	inositol 1,4,5-triphosphate receptor, type 2
703964	-0.5620699	inositol polyphosphate phosphatase-like 1
180803	-0.621787	inositol polyphosphate-1-phosphatase
77533	0.3205713	inositol polyphosphate-5-phosphatase, 40kD
207288	0.603346	insulin induced gene 1
814350	0.588877	insulin-degrading enzyme
753620	-0.5248489	insulin-like growth factor binding protein 6
471196	-0.7192268	integral membrane protein 3
785530	-0.5600048	integrin, alpha 1
188388	-0.6824191	integrin, alpha 10

32493	-0.7093777	integrin, alpha 6
130201	-1.0401997	intercellular adhesion molecule 2
755599	0.3413351	interferon induced transmembrane protein 1 (9-27)
1159963	0.4323117	interferon regulatory factor 7
782513	0.4759571	interferon, alpha-inducible protein (clone IFI-6-16)
824602	-0.5107682	interferon, gamma-inducible protein 16
154493	0.3629466	interferon-induced protein 75, 52kD
84295	0.3989864	interleukin 1 receptor antagonist
491763	-0.679034	interleukin 1, beta
811920	-1.2690713	interleukin 11 receptor, alpha
1517171	0.5195255	interleukin 2 receptor, alpha
80344	-0.8243418	interleukin 7 receptor
859228	0.5817344	isocitrate dehydrogenase 1 (NADP+), soluble
869375	0.4827093	isocitrate dehydrogenase 2 (NADP+), mitochondrial
868128	0.7347171	JM4 protein
414992	0.420994	K562 cell-derived leucine-zipper-like protein 1
344588	-0.55146	kallikrein 5
809784	-0.7095414	kallikrein 6 (neurosin, zyme)
2243051	-0.7736287	kallikrein 8 (neuropsin/ovasin)
824962	0.4638758	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
852829	0.3691079	karyopherin alpha 3 (importin alpha 4)
625234	0.550211	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
1474900	-0.736252	keratin 15
344988	0.3464047	<b>keratin, hair, acidic, Homo sapiens</b>
773922	0.6730903	KIAA0005 gene product
686172	0.6724684	KIAA0008 gene product
1350439	-0.6740833	KIAA0015 gene product
788444	0.4042598	KIAA0033 protein
814054	0.7539407	KIAA0040 gene product
725223	0.4167519	KIAA0077 protein
898032	0.7216	KIAA0097 gene product
841501	0.4111707	KIAA0102 gene product
530310	0.4739401	KIAA0143 protein
415191	-0.512457	KIAA0161 gene product
812975	-0.6921755	KIAA0172 protein
79710	0.4579008	KIAA0174 gene product
1517595	0.3804132	KIAA0175 gene product
43977	0.3961848	KIAA0182 protein
1473471	-0.9623482	KIAA0194 protein
49117	0.4856399	KIAA0215 gene product

1584287 0.4413331 KIAA0241 protein  
782428 0.701077 KIAA0250 gene product  
1884404 0.5849803 KIAA0285 gene product  
2028238 -0.6141182 KIAA0300 protein  
809944 0.6530236 KIAA0310 gene product  
795805 0.4370764 KIAA0332 protein  
773426 0.3727398 KIAA0391 gene product  
752668 -0.65723 KIAA0440 protein  
221499 0.4149929 KIAA0508 protein  
1910316 0.3498986 KIAA0535 gene product  
753162 -0.7617972 KIAA0603 gene product  
725841 0.561197 KIAA0662 gene product  
1636166 -0.8845211 KIAA0668 protein  
180785 0.322529 KIAA0726 gene product  
786265 0.3760397 KIAA0750 gene product  
40173 0.5940582 KIAA0807 protein  
460126 -0.5320146 KIAA0819 protein  
26171 0.3656147 KIAA0856 protein  
35300 -0.688788 KIAA0869 protein  
1679942 0.3706798 KIAA1053 protein  
277044 -0.6947855 KIAA1183 protein  
124447 0.6918546 KIAA1184 protein  
771004 -0.5144276 KIAA1201 protein  
1843843 0.3290269 KIAA1304 protein  
1518402 0.5497179 KIAA1361 protein  
345056 -0.6863529 KIAA1404 protein  
788558 -0.5600825 KIAA1479 protein  
843054 0.4637278 KIAA1533 protein  
50586 -0.6794282 KIAA1545 protein  
812959 -0.5591846 KIAA1638 protein  
1881774 -0.5265891 KIAA1678  
149539 0.4138942 KIAA1700  
277571 -0.9841522 KIAA1706 protein  
703541 -0.5534921 KIAA1858 protein  
753038 -0.893161 kinesin family member C3  
825606 0.335057 kinesin-like 1  
769942 0.3810371 kinesin-like 4  
343731 0.3962504 **Kruppel-like factor 2 (lung) (KLF2), Homo sapiens**  
132711 -0.7962294 Kruppel-like factor 5 (intestinal)  
280249 0.4096162 Kruppel-like factor 7 (ubiquitous)  
280907 -0.7307519 Kruppel-type zinc finger protein  
795178 -0.5169102 lactate dehydrogenase C  
346545 -0.7887371 laminin, beta 1  
460403 -0.5739604 laminin, gamma 2 (nicein (100kD), kalinin (105kD), BM600  
(100kD), Herlitz junctional epidermolysis bullosa))

770355 0.5518948 lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)  
767202 -1.0654145 latent transforming growth factor beta binding protein 2  
897731 -0.6670507 latrophilin  
199403 0.7754748 lectin, galactoside-binding, soluble, 8 (galectin 8)  
774078 -0.6508021 leiomodin 1 (smooth muscle)  
60565 0.4659865 lethal giant larvae (*Drosophila*) homolog 2  
470092 0.476018 like-glycosyltransferase  
1160723 -0.5005952 LIM domain kinase 2  
712829 -0.5797871 LIM domain only 2 (rhombotin-like 1)  
2056139 -1.0673271 LIM domain protein  
247616 -0.6585351 lipoma HMGIC fusion partner  
1469377 -1.2127781 lipoma HMGIC fusion partner-like 2  
868169 -0.5584677 lipoprotein lipase  
810947 0.3833137 LIS1-interacting protein NUDE1, rat homolog  
825296 0.4646099 low density lipoprotein receptor defect C complementing  
490778 0.5932928 low molecular mass ubiquinone-binding protein (9.5kD)  
341759 -0.5403406 lung type-I cell membrane-associated glycoprotein  
150314 0.5114988 lysophospholipase I  
826363 0.5823873 lysophospholipase II  
840942 -0.6383764 major histocompatibility complex, class II, DP beta 1  
1592530 -0.5918818 mammalian inositol hexakisphosphate kinase 2  
366100 -0.6885372 matrilin 2  
470393 -0.830751 matrix metalloproteinase 7 (matrilysin, uterine)  
142586 0.4942961 MCT-1 protein  
2069602 0.3539588 melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)  
346688 -0.5315035 melanoma inhibitory activity  
200814 -1.4325283 membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)  
296880 -0.6655878 membrane protein, palmitoylated 1 (55kD)  
729975 0.7649717 meningioma expressed antigen 5 (hyaluronidase)  
1472735 -0.5888169 metallothionein 1E (functional)  
1518890 0.5314577 metallothionein-like 5, testis-specific (tesmin)  
878406 0.4396935 metaxin 1

2014034 0.6620303 methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase

124298 0.4922937 microsomal glutathione S-transferase 3

133518 -0.6817662 microtubule-associated protein, RP/EB family, member 2

564492 0.5626905 mitochondrial carrier homolog 2

491524 0.3785047 mitochondrial ribosomal protein L13

321354 0.3489273 mitochondrial ribosomal protein L15

2019223 0.5663073 mitochondrial ribosomal protein L17

788334 0.5347204 mitochondrial ribosomal protein L23

416436 0.3325571 mitochondrial ribosomal protein L24

417801 0.4112944 mitochondrial ribosomal protein L27

782608 0.6137782 **mitochondrial ribosomal protein L9**

782608 0.6978285 mitochondrial ribosomal protein L9

1909574 0.3900357 mitochondrial ribosomal protein S11

70201 -0.6675012 mitochondrial solute carrier

590774 0.5460342 mitogen-activated protein kinase 13

767641 -0.5881449 mitogen-activated protein kinase 8 interacting protein 2

1358393 -0.5090372 mitogen-activated protein kinase kinase 3

342349 -0.603487 mitogen-activated protein kinase kinase kinase 14

2326057 0.5310995 MLN51 protein

154707 0.3831976 MpV17 transgene, murine homolog, glomerulosclerosis

530093 0.3463461 myelin protein zero-like 1

611443 0.5432426 myoglobin

470128 -0.5253542 myosin IE

1473274 -1.1172693 myosin regulatory light chain 2, smooth muscle isoform

712314 0.3338146 myosin regulatory light chain interacting protein

629944 0.5273447 myosin VB

744944 0.4769116 myosin VI

841308 -0.9953716 myosin, light polypeptide kinase

840865 0.4666048 myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)

1456348 0.6417276 N-acetylneuraminic acid phosphate synthase; sialic acid synthase

66599 0.3561699 N-acetyltransferase 1 (arylamine N-acetyltransferase)

1635681 0.6022549 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (8kD, B8)

951216 0.4594172 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)

487733 0.5057167 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2  
(8kD, AGGG)  
487733 0.6262778 **NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2**  
**(8kD, AGGG)**  
753457 0.3515361 NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD)  
(NADH-coenzyme Q reductase)  
358609 0.4071867 NADH dehydrogenase (ubiquinone) flavoprotein 3 (10kD)  
172785 0.3493683 NAG-5 protein  
1762111 0.4160469 natriuretic peptide receptor C/guanylate cyclase C  
(atropinatriuretic peptide receptor C)  
76605 0.6484522 nesca protein  
773381 0.3525581 N-ethylmaleimide-sensitive factor attachment protein, alpha  
52076 0.3633002 neuroblastoma (nerve tissue) protein  
838478 -1.1175047 neurocalcin delta  
289428 -0.7270494 neurotrophic tyrosine kinase, receptor, type 2  
877621 -1.1501074 nGAP-like protein  
306798 -0.8718483 NGFI-A binding protein 1 (EGR1 binding protein 1)  
199645 0.5334951 nicastrin  
85840 -0.7754435 nicotinamide N-methyltransferase  
811761 0.6045809 Nijmegen breakage syndrome 1 (nibrin)  
269606 0.3228482 N-methylpurine-DNA glycosylase  
825659 0.424655 N-myc downstream regulated  
842863 0.3225116 N-myc downstream regulated  
75859 -1.8328232 N-myc downstream-regulated gene 2  
845363 0.4570873 non-metastatic cells 1, protein (NM23A) expressed in  
726658 0.4446657 non-metastatic cells 3, protein expressed in  
203003 0.5743416 non-metastatic cells 4, protein expressed in  
131091 0.3548154 Not56 (D. melanogaster)-like protein  
789382 -0.6898974 Notch (Drosophila) homolog 4  
795256 0.5567908 NPD007 protein  
754040 -0.610807 NS1-associated protein 1  
42831 0.3638165 N-terminal kinase-like  
1637516 0.325364 nuclear autoantigen  
703739 0.392298 nuclear cap binding protein subunit 1, 80kD  
207794 0.3679245 nuclear factor (erythroid-derived 2), 45kD  
345069 0.3532976 nuclear factor (erythroid-derived 2)-like 3  
416959 -0.957248 nuclear factor I/B

503851 0.5170168 nuclear receptor co-repressor/HDAC3 complex subunit  
823714 -0.642903 nuclear receptor co-repressor/HDAC3 complex subunit  
773188 0.5454398 nuclear receptor subfamily 1, group D, member 2  
377384 0.4698441 nuclear receptor subfamily 2, group F, member 2  
815794 0.3643266 nucleobindin 2  
1600281 0.3304323 nucleolar protein 3 (apoptosis repressor with CARD domain)  
843070 -0.6925728 nucleoporin 88kD  
811808 0.326728 nucleoside diphosphate kinase type 6 (inhibitor of p53-induced apoptosis-alpha)  
42681 -0.5388424 NY-REN-25 antigen  
773674 0.4601667 oncogene TC21  
1523225 0.4195302 oncostatin M receptor  
504461 0.3506753 opsin 3 (encephalopsin)  
155896 -0.5182247 ORF  
66535 0.5363248 ornithine decarboxylase antizyme 2  
1533710 -0.5988282 ortholog of mouse integral membrane glycoprotein LIG-1  
2028722 -0.8800075 osteoblast specific factor 2 (fasciclin I-like)  
1753497 0.409432 ovo (Drosophila) homolog-like 1  
111362 0.4045961 oxysterol binding protein-like 2 (OSBPL2),  
756442 0.5313744 P450 (cytochrome) oxidoreductase  
781019 0.5918462 paraoxonase 2  
81203 0.3328573 paraoxonase 3  
1404774 -0.5685596 parathyroid hormone-like hormone  
785368 0.3254362 PDZ-binding kinase; T-cell originated protein kinase  
1882697 -1.4318896 peanut (Drosophila)-like 2  
416676 -0.9140494 pellino (Drosophila) homolog 1  
285377 -1.3699153 pellino (Drosophila) homolog 2  
1631132 0.401216 peptide transporter 3  
1631682 -0.5162406 peptidylprolyl isomerase E (cyclophilin E)  
1587710 -0.8252065 period (Drosophila) homolog 1  
1573251 0.6410435 peroxisomal long-chain acyl-coA thioesterase  
788518 -0.5697316 peroxisomal membrane protein 3 (35kD, Zellweger syndrome)  
814353 0.3622592 phorbol-12-myristate-13-acetate-induced protein 1  
897963 -0.9775616 phosphatidic acid phosphatase type 2A  
85394 -0.4913773 phosphatidic acid phosphatase type 2B  
346942 0.4657601 phosphatidylinositol glycan, class Q

788136 -0.7778375 phosphodiesterase 4B, cAMP-specific (dunce (*Drosophila*)-homolog phosphodiesterase E4)  
773685 0.4009493 phosphodiesterase 4D interacting protein (myomegalin)  
625923 0.5839066 phosphoenolpyruvate carboxykinase 2 (mitochondrial)  
897177 0.3712716 phosphoglycerate mutase 1 (brain)  
712401 -0.9068788 phosphoinositide-3-kinase, catalytic, delta polypeptide  
811779 -0.5291718 phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)  
811142 0.3361932 phosphoinositide-3-kinase, regulatory subunit, polypeptide 2 (p85 beta)  
272529 0.7486269 phosphomannomutase 2  
725284 0.4992842 phosphorylase kinase, gamma 2 (testis)  
1474337 -0.7766266 phosphorylase, glycogen; brain  
843195 0.8603524 phosphoserine phosphatase  
503215 0.9108688 pilin-like transcription factor  
586803 -0.7423407 placental growth factor, vascular endothelial growth factor-related protein  
814815 -0.5675649 plakophilin 4  
66491 -0.9280245 plasmolipin  
1568391 -0.5467858 plastin 3 (T isoform)  
810124 0.6162712 platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)  
52096 -0.6789228 platelet-derived growth factor receptor, alpha polypeptide  
365358 0.5883524 pM5 protein  
290378 -0.7751825 podocalyxin-like  
859761 0.6573769 poliovirus receptor-related 2 (herpesvirus entry mediator B)  
744047 0.4151137 polo (*Drosophila*)-like kinase  
75059 -0.5504962 poly(A)-binding protein, cytoplasmic 1-like  
897813 0.4749348 polyadenylate binding protein-interacting protein 1  
741769 0.3475255 polymerase (DNA directed), beta  
810734 0.4998276 polymerase (DNA-directed), delta 4  
813410 0.5513568 polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)  
1325816 0.4379227 polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)  
814270 0.3300091 polymyositis/scleroderma autoantigen 1 (75kD)  
756708 -0.910505 potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4  
67741 -1.0705249 PP2135 protein

69002 -0.9960916 PPAR(gamma) angiopoietin related protein  
  
241348 0.7324115 prenylcysteine lyase  
284592 -0.5205573 PRO1659 protein  
280375 0.8392836 PRO2000 protein  
263013 0.3894536 procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2  
2020898 0.4797032 procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3  
  
486110 0.4017126 profilin 2  
41698 0.4310061 progesterone binding protein  
2161427 0.3509243 progesterone receptor  
837864 0.3314764 progestin induced protein  
1573946 0.5173691 programmed cell death 9  
470035 0.3436575 prokineticin 1 precursor  
138788 0.5302936 prolactin receptor  
837870 -0.657186 proline arginine-rich end leucine-rich repeat protein  
  
855800 0.4748367 prolyl endopeptidase  
27544 -0.708383 prominin (mouse)-like 1  
2213824 -0.5412089 protease inhibitor 3, skin-derived (SKALP)  
307687 -0.5106552 protease, serine, 16 (thymus)  
810558 0.6698194 proteasome (prosome, macropain) 26S subunit, ATPase, 4  
  
2050827 0.5544641 proteasome (prosome, macropain) 26S subunit, ATPase, 5  
  
1553306 0.5344506 proteasome (prosome, macropain) 26S subunit, non-ATPase, 11  
823598 0.9153521 proteasome (prosome, macropain) 26S subunit, non-ATPase, 12  
2054635 0.7914755 proteasome (prosome, macropain) subunit, alpha type, 7  
122241 0.7394284 proteasome (prosome, macropain) subunit, beta type, 2  
951233 0.5767874 proteasome (prosome, macropain) subunit, beta type, 3  
1460110 0.5392177 proteasome (prosome, macropain) subunit, beta type, 5  
1473289 0.674396 protective protein for beta-galactosidase (galactosialidosis)  
26883 0.4103824 protein kinase (cAMP-dependent, catalytic) inhibitor beta  
591055 -0.5258289 protein kinase C and casein kinase substrate in neurons 2  
755301 0.3749416 protein kinase C, delta  
2055807 0.5460123 protein kinase domains containing protein similar to phosphoprotein C8FW

205049 0.5734444 protein kinase H11; small stress protein-like protein HSP22  
756666 0.4835569 protein phosphatase 1, catalytic subunit, alpha isoform  
814989 0.3426862 protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform  
41356 0.4746307 protein phosphatase 2, regulatory subunit B (B56), alpha isoform  
358162 0.4901786 protein predicted by clone 23627  
785707 0.4708376 protein regulator of cytokinesis 1  
73638 0.3425644 protein tyrosine phosphatase type IVA, member 2  
774502 0.3402891 protein tyrosine phosphatase, non-receptor type 12  
83363 0.6526164 protein-L-isoaspartate (D-aspartate) O-methyltransferase  
26566 -0.7278186 protein-O-mannosyltransferase 1  
303109 -0.9414602 purinergic receptor (family A group 5)  
141852 0.4748862 purinergic receptor P2Y, G-protein coupled, 2  
1917941 0.8340565 purine-rich element binding protein B  
744374 0.4824256 putative ankyrin-repeat containing protein  
685516 0.8762873 putative G protein-coupled receptor  
122077 0.9021901 putative membrane protein  
261472 0.4941066 putative nuclear protein ORF1-FL49  
795498 0.4270889 putative transmembrane protein  
80374 -0.5236475 pyruvate dehydrogenase (lipoamide) alpha 1  
826077 0.4242762 pyruvate dehydrogenase (lipoamide) beta  
365060 0.4976091 RAB11A, member RAS oncogene family  
79520 0.6769129 RAB2, member RAS oncogene family  
1911343 0.9116745 RAB26, member RAS oncogene family  
1639531 0.4658349 RAB27A, member RAS oncogene family  
248886 -0.5823315 rab3 GTPase-activating protein, non-catalytic subunit (150kD)  
784150 0.4702303 RAB31, member RAS oncogene family  
785701 0.5446211 RAB31, member RAS oncogene family  
1845169 0.5588842 RAB35, member RAS oncogene family  
2009779 0.420743 rabaptin-5  
687990 -0.5253354 Rac/Cdc42 guanine exchange factor (GEF) 6  
470124 0.6641768 RAD1 (*S. pombe*) homolog  
1476053 0.5179015 RAD51 (*S. cerevisiae*) homolog (*E. coli* RecA homolog)  
1686766 -0.7192745 Rag D protein  
505864 -0.7677235 RalGDS-like gene  
143426 0.3764075 ras homolog gene family, member B  
2316441 -0.6206597 ras homolog gene family, member C

725308 -0.6371261 ras inhibitor  
80727 -0.7538606 receptor tyrosine kinase-like orphan receptor 1  
45099 -1.3515907 regucalcin (senescence marker protein-30)  
  
2106144 -1.067765 regulated in glioma  
1500542 0.3228485 regulator of G-protein signalling 11  
813707 0.410787 regulator of G-protein signalling 16  
2017403 0.3211799 regulator of G-protein signalling 3  
383501 -0.502319 regulator of G-protein signalling 9  
309288 0.334016 replication factor C (activator 1) 4 (37kD)  
204299 0.4073087 replication protein A3 (14kD)  
898253 0.3331924 reticulocalbin 2, EF-hand calcium binding domain  
  
685185 -0.5172158 reticulon 2  
781097 0.7126945 reticulon 3  
2322367 0.5832711 reticulon 4  
595037 0.990461 retinoic acid induced 3  
756372 -0.5447652 retinoic acid receptor responder (tazarotene induced) 2  
  
812994 0.4854155 retinoid X receptor, alpha  
810959 0.3534647 Rho GDP dissociation inhibitor (GDI) alpha  
  
244801 0.8066357 Rho guanine exchange factor (GEF) 11  
1422338 0.5874097 ribonucleotide reductase M2 polypeptide  
869450 -0.7659922 ribosomal protein L11  
990881 -0.8335353 **ribosomal protein L12 (Rpl12), mus musculus**  
814316 -0.9276916 ribosomal protein L13  
307029 -0.6500872 ribosomal protein L26  
1630990 -0.7312981 ribosomal protein L29  
322561 -0.7970805 ribosomal protein L31  
178137 -0.6839022 ribosomal protein L34  
877835 -0.5382125 ribosomal protein L35  
415233 -0.6506593 ribosomal protein L37a  
51981 -0.5554908 ribosomal protein L7a  
123441 0.4862068 ribosomal protein L7a  
2252417 -0.6222381 ribosomal protein S10  
772898 0.372064 ribosomal protein S15a  
868308 -0.5157133 ribosomal protein S23  
1637296 -0.5105214 ribosomal protein S24  
1475738 -0.6753091 ribosomal protein S25  
877827 -0.7093855 ribosomal protein S27a  
1492147 -0.636656 ribosomal protein S4, X-linked  
309449 -0.5401954 ribosomal protein S4, Y-linked  
322233 -0.5578912 ribosomal protein, large, P0  
469686 0.8919992 Ric (Drosophila)-like, expressed in many tissues

1636844 0.3926235 ring finger protein 14  
200144 0.4019827 ring-box 1  
133236 -0.8888316 RNA binding motif protein, X chromosome  
746373 -0.5513143 RNA polymerase I transcription factor RRN3

813845 0.3637519 RNA, U transporter 1  
291478 -1.0212528 runt-related transcription factor 3  
756595 0.395121 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))

810612 0.6341098 S100 calcium-binding protein A11 (calgizzarin)

824108 0.3381616 SCAN domain-containing 1  
416434 -0.8006527 SCN Circadian Oscillatory Protein (SCOP)  
785840 0.5401209 SEC24 (*S. cerevisiae*) related gene family, member D

358456 0.4812268 Sec61 gamma  
2306987 0.4402912 secreted and transmembrane 1  
270917 -0.6918383 secreted frizzled-related protein 1  
250654 -0.5815576 secreted protein, acidic, cysteine-rich (osteonectin)

2284803 -0.6265431 secretory carrier membrane protein 1  
878836 -1.037352 secretory granule, neuroendocrine protein 1 (7B2 protein)

378813 -0.7346408 secretory leukocyte protease inhibitor (antileukoproteinase)

840878 0.5648009 seladin-1  
1609625 -0.5920312 selectin P ligand  
1492463 0.8634521 selenoprotein X, 1  
327432 -0.4870045 semaphorin Y  
207735 -0.7167416 serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1

592801 0.3638731 serine palmitoyltransferase, long chain base subunit 2

814378 0.6317382 serine protease inhibitor, Kunitz type, 2  
209066 0.5794211 serine/threonine kinase 15  
209066 0.6611038 **serine/threonine kinase 15**  
271899 0.355689 Ser-Thr protein kinase related to the myotonic dystrophy protein kinase

161456 -0.8215502 serum amyloid A1  
1917449 -1.0894686 serum amyloid A4, constitutive  
159462 -0.528299 serum constituent protein  
470061 0.77977 seven in absentia (*Drosophila*) homolog 2  
813631 0.534683 seven transmembrane protein TM7SF3  
49351 0.6386132 SEX gene  
343760 -0.6724144 SH3 domain binding glutamic acid-rich protein like 2

2302099 0.5813788 sialidase 3 (membrane sialidase)  
813751 0.5051993 sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase)  
785616 0.6484744 signal sequence receptor, alpha (translocon-associated protein alpha)  
2504881 -1.000863 signal transducer and activator of transcription 5A  
144740 0.4449229 similar to phosphatidylcholine transfer protein 2  
345034 -1.0600859 small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)  
140574 -0.9652218 small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)  
2322223 0.3853156 small nuclear ribonucleoprotein polypeptide A  
704414 0.6940045 small nuclear ribonucleoprotein polypeptides B and B1  
288999 0.6938843 small protein effector 1 of Cdc42  
1692195 0.3254467 smg GDS-ASSOCIATED PROTEIN  
530958 -0.7809384 smoothened (Drosophila) homolog  
810762 0.4806851 SNARE protein  
472103 0.4043572 soc-2 (suppressor of clear, C.elegans) homolog  
2054122 0.3318413 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3  
755855 -0.6298333 solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6  
49273 0.5691181 solute carrier family 27 (fatty acid transporter), member 4  
1568126 0.3434836 solute carrier family 37 (glycerol-3-phosphate transporter), member 1  
1702742 0.5011725 solute carrier family 7 (cationic amino acid transporter, y+ system), member 5  
289936 0.3382708 solute carrier family 7, (cationic amino acid transporter, y+ system) member 11  
773286 0.3861543 solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1  
2413337 -0.4879268 sortilin-related receptor, L(DLR class) A repeats-containing  
823871 -0.9429443 SPARC-like 1 (mast9, hevin)  
815142 -0.4881454 spastic ataxia of Charlevoix-Saguenay (sacsin)  
345764 -0.5504113 special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)

76362	0.3349202	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
1734309	0.5894492	sperm associated antigen 4
503866	0.4230404	sperm autoantigenic protein 17
565235	0.4124667	spermine synthase
1626304	-0.7769866	spinal cord-derived growth factor-B
813698	-0.4898644	sprouty ( <i>Drosophila</i> ) homolog 2
124781	0.6324418	squalene epoxidase
1558675	-1.3749762	SRY (sex determining region Y)-box 10
1469425	0.8296141	SRY (sex determining region Y)-box 22
768571	-0.8572018	SRY (sex determining region Y)-box 8
2306752	-0.5123647	stathmin-like 2
25440	0.3554359	staufen ( <i>Drosophila</i> , RNA-binding protein) homolog 2
2018084	0.6119069	Ste-20 related kinase
302031	0.5111067	Ste20-related serine/threonine kinase
810711	0.9128832	stearoyl-CoA desaturase (delta-9-desaturase)
590759	0.4895021	sterol-C4-methyl oxidase-like
154466	0.3258377	STIP1 homology and U-Box containing protein 1
595070	0.3408109	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4
35191	0.3427094	stromal cell-derived factor 2
366132	1.013995	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
125342	-0.5078237	SUMO-1-specific protease
781014	-1.0161379	suppression of tumorigenicity 5
785933	-0.5340762	sushi-repeat-containing protein, X chromosome
418159	-0.7545888	synaptogyrin 1
969877	0.707469	synaptosomal-associated protein, 25kD
177827	0.3691459	synaptotagmin VII
826194	0.4177687	synaptotagmin-like 2
135640	0.3288537	syntaxin 3A
509588	0.4157059	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD
1474955	0.6045103	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
490102	-0.5383385	TBP-associated factor 172
366591	-0.7595643	T-cell lymphoma invasion and metastasis 2
726637	0.3292392	t-complex-associated-testis-expressed 1-like

1631194 0.3219004 t-complex-associated-testis-expressed 1-like 1  
346696 0.3570344 TEA domain family member 4  
47043 -0.7729643 tensin  
454339 0.3738929 thiopurine S-methyltransferase  
782193 -0.5788147 thioredoxin  
795543 0.3500184 thioredoxin peroxidase (antioxidant enzyme)  
789376 0.4339171 thioredoxin reductase 1  
965223 0.3642603 thymidine kinase 1, soluble  
739126 0.4905859 tissue specific transplantation antigen P35B  
825470 0.5218731 topoisomerase (DNA) II alpha (170kD)  
1591264 0.3849595 transaldolase 1  
347373 0.7563599 transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)  
725680 -0.7197488 transcription factor AP-2 gamma (activating enhancer-binding protein 2 gamma)  
713839 -0.5080365 transcription factor AP-4 (activating enhancer-binding protein 4)  
823940 0.4214277 transducer of ERBB2, 1  
1473131 -0.5594101 transducin-like enhancer of split 2, homolog of Drosophila E(sp1)  
240248 -0.5660209 transferrin  
705064 0.4497555 transforming, acidic coiled-coil containing protein 3  
882248 -0.8700731 transgelin  
878421 -0.5233873 transgelin 2  
359887 0.8692353 translocase of inner mitochondrial membrane 17 (yeast) homolog A  
149355 0.6520333 translocating chain-associating membrane protein  
826256 0.7190206 transmembrane 7 superfamily member 1 (upregulated in kidney)  
298417 0.3833014 trefoil factor 3 (intestinal)  
855749 0.476968 triosephosphate isomerase 1  
42076 0.3194462 TRK-fused gene  
897720 -0.5904719 trophinin  
740620 -0.96496 tropomyosin 2 (beta)  
611532 -1.3158379 troponin I, skeletal, fast  
1409509 0.554703 troponin T1, skeletal, slow  
489657 0.3847527 tryptophan rich basic protein  
757489 0.4859039 tubulin, alpha 2  
825585 0.5722829 tubulin-specific chaperone e  
1665444 -0.651994 tumor endothelial marker 1 precursor

142259 -0.8376566 tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; Huntingtin interacting protein L; transcription factor IIIA-interacting protein

491403 -0.7700599 tumor necrosis factor receptor superfamily, member 1B

714213 -0.5129593 tumor necrosis factor receptor superfamily, member 6

814306 0.4705205 tumor protein D52

1435003 0.6457486 tumor suppressing subtransferable candidate 1

1856063 -0.8833091 tweety (Drosophila) homolog 1

292996 0.36439 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide

868396 -0.808677 tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide

626318 0.4529715 ubinuclein 1

1908834 -0.7177051 ubiquitin A-52 residue ribosomal protein fusion product 1

769921 0.6464245 ubiquitin carrier protein E2-C

81599 0.3932769 ubiquitin specific protease 14 (tRNA-guanine transglycosylase)

745083 0.4107735 ubiquitin specific protease 18

795288 -0.6528792 ubiquitin specific protease 4 (proto-oncogene)

250883 -0.7925068 ubiquitin-activating enzyme E1-like

1698036 0.5298397 ubiquitin-conjugating enzyme E2 variant 1

839682 0.5208954 ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)

843094 -0.5617478 ubiquitin-like 1 (sentrin)

289978 0.6308861 ubiquitin-like 4

713862 0.3965573 ubiquitin-protein isopeptide ligase (E3)

824524 0.4375695 UDP-galactose transporter related

150897 -0.6188264 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3

139835 0.5253386 UDP-glucose dehydrogenase

809727 0.365892 unc-51 (C. elegans)-like kinase 1

284261 0.6890531 uncharacterized hematopoietic stem/progenitor cells protein MDS030

1471829 -0.7275378 uncharacterized hypothalamus protein HSMNP1

884498 0.4648731 uncharacterized hypothalamus protein HT012

236034 0.7039329 uncoupling protein 2 (mitochondrial, proton carrier)

783681 0.354881 upstream regulatory element binding protein 1

769600 0.4362014 uracil-DNA glycosylase 2  
1912951 0.329484 uterine-derived 14 kDa protein  
81336 0.4955353 uteroglobin  
1631699 0.6027911 valosin-containing protein  
855061 -0.5203046 vascular endothelial growth factor B  
240620 -0.5065007 vascular Rab-GAP/TBC-containing  
215000 -0.555725 vasoactive intestinal peptide receptor 1  
810057 -0.6178096 vasoactive intestinal peptide receptor 1  
202901 0.48608 vav 2 oncogene  
855563 0.5059683 v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3  
810316 0.3732635 very long-chain acyl-CoA synthetase; lipidosin  
  
1161775 -0.7380353 villin 1  
840511 -0.6341661 vimentin  
358531 -0.5784457 v-jun avian sarcoma virus 17 oncogene homolog  
  
71087 -0.8416951 v-maf musculoaponeurotic fibrosarcoma (avian) oncogene family, protein F  
290866 -0.5467613 v-raf-1 murine leukemia viral oncogene homolog 1  
  
322617 0.3623149 v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)  
  
193913 -0.6425581 v-yes-1 Yamaguchi sarcoma viral related oncogene homolog  
  
784140 0.474314 WD repeat domain 15  
731023 0.4853217 WD repeat domain 5  
268946 0.5440003 WD40 protein Ciao1  
2306221 0.4068933 wingless-type MMTV integration site family, member 10B  
  
235986 0.338857 wingless-type MMTV integration site family, member 11  
  
138189 0.9386802 Wolfram syndrome 1 (wolframin)  
813281 0.7092607 WW domain-containing protein 1  
795185 0.5276861 xenotropic and polytropic retrovirus receptor  
  
813629 0.6549767 YME1 (*S.cerevisiae*)-like 1  
147834 0.4412795 zinc finger protein 217  
209537 -0.763749 zinc finger protein 221  
82421 0.3506778 zinc finger protein 6 (CMPX1)

**Table 5** (in alphabetical order)

CloneID	Weight	Description
770785	0.658751	1,2-alpha-mannosidase IC

1574058	0.9058211	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)
713782	0.6552297	a disintegrin and metalloproteinase domain 15 (metarginidin)
488505	0.7242619	accessory proteins BAP31/BAP29
823930	0.6738266	actin related protein 2/3 complex, subunit 1A (41 kD)
1473922	0.7399948	actin related protein 2/3 complex, subunit 3 (21 kD)
340558	0.7990715	actin related protein 2/3 complex, subunit 5 (16 kD)
210862	0.7483198	acyl-Coenzyme A oxidase 1, palmitoyl
343607	0.6510034	AD-015 protein
51532	0.7195798	ADP-ribosylation factor-like 6 interacting protein
712139	-1.1491129	ADP-ribosylation factor-like 7
46248	0.9628117	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)
248631	-1.0784377	aminomethyltransferase (glycine cleavage system protein T)
208718	-1.0229324	annexin A1
1435862	0.723081	antigen identified by monoclonal antibodies 12E7, F21 and O13
2110511	0.7863117	artemin
377275	-1.3392122	ataxia-telangiectasia group D-associated protein
810725	0.7561061	ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 21kD
796694	1.1580364	baculoviral IAP repeat-containing 5 (survivin)
1709791	0.8397779	BAI1-associated protein 1
1456701	0.6383709	B-cell CLL/lymphoma 9
2043167	0.8551193	BCL2-associated athanogene 3
1420370	0.7726877	biliverdin reductase B (flavin reductase (NADPH))
811024	0.6706275	bone marrow stromal cell antigen 2
1616253	0.7231756	breast carcinoma amplified sequence 1
754653	0.62777098	cadherin, EGF LAG seven-pass G-type receptor 3, flamingo ( <i>Drosophila</i> ) homolog
67765	0.7064266	carboxypeptidase M
509823	0.6982362	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
744417	0.6975761	carnitine acetyltransferase
72778	-1.3299927	caspase 7, apoptosis-related cysteine protease
1878409	-1.013872	catechol-O-methyltransferase

842994	0.7983201	cathepsin Z
377461	-1.3214357	caveolin 1, caveolae protein, 22kD
725454	0.9476507	CDC28 protein kinase 2
786067	0.7228184	cell division cycle 25B
415102	0.6562436	cell division cycle 25C
2017415	0.7281714	centromere protein A (17kD)
2108077	0.6796871	CGI-112 protein
753400	0.6633015	CGI-204 protein
811774	0.9014801	CGI-49 protein
624667	0.9336899	CGI-92 protein
884425	0.6608337	chaperonin containing TCP1, subunit 5 (epsilon)
1492426	0.8032542	chromosome 19 open reading frame 3
469383	0.6925975	chromosome 8 open reading frame 1
124331	0.7081481	cleavage and polyadenylation specific factor 5, 25 kD subunit
770992	0.693225	<b>contig C056172, human</b>
897770	0.715754	<b>contig C071196, human</b>
108425	0.7581954	<b>contig C076797, human</b>
119290	-1.025797	cortic al thymocyte receptor (X. laevis CTX) like
839736	-1.2337192	crystallin, alpha B
742595	0.6784804	cyclin-dependent kinase 5
700792	0.8005506	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)
1323448	1.1309009	cysteine-rich protein 1 (intestinal)
278531	0.6404612	cytochrome c oxidase subunit VIc
1601947	0.6297475	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
768064	0.6936336	cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 1
810156	0.6879064	deoxythymidylate kinase (thymidylate kinase)
1161564	-1.5877154	desmuslin
842980	0.762412	developmentally regulated GTP-binding protein 1
760299	-1.8441097	dickkopf (Xenopus laevis) homolog 3
742685	-1.248683	disabled (Drosophila) homolog 2 (mitogen-responsive phosphoprotein)
825740	0.6805157	DKFZp434J1813 protein
1635062	-0.9905245	DKFZP586A011 protein
2011515	0.6319712	DKFZP586B0923 protein
454896	0.6384516	DnaJ (Hsp40) homolog, subfamily A, member 2
593023	-1.0158099	dystrobrevin, beta
781017	-1.0125987	early growth response 2 (Krox-20 (Drosophila) homolog)

366834	0.629867	envoplakin
153760	-1.0340645	EphB1
811088	-1.140941	ephrin-B3
109863	0.683291	epithelial membrane protein 2
358267	0.6648183	EST, Moderately similar to AF119917 63 PRO2831 [H.sapiens]
160609	-1.0208819	ESTs
196435	-1.1475545	ESTs
344091	0.6818771	ESTs
365738	0.7152855	ESTs
564847	0.6770455	ESTs
564981	0.7745626	ESTs
754628	0.9061145	ESTs
757191	-1.0238476	ESTs
784105	0.6244805	ESTs
827171	0.7543905	ESTs
1257131	-0.9869928	ESTs
1500162	0.8155519	ESTs
1536006	0.6805004	ESTs
431505	0.6840493	ESTs, Highly similar to A31026 probable membrane receptor protein [H.sapiens]
289760	-1.2610055	ESTs, Highly similar to T00391 hypothetical protein KIAA0612 [H.sapiens]
593431	0.6422897	ESTs, Moderately similar to CEGT_HUMAN CERAMIDE GLUCOSYLTRANSFERASE [H.sapiens]
345670	-1.2805684	ESTs, Moderately similar to I59348 CCAAT binding transcription factor CBF subunit C - rat [R.norvegicus]
529843	-1.0698218	ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]
120749	0.7545697	ESTs, Moderately similar to KIAA1215 protein [H.sapiens]
160192	-1.4231519	ESTs, Weakly similar to 2004399A chromosomal protein [H.sapiens]
73009	0.731401	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
2016908	0.969649	ESTs, Weakly similar to CA13_HUMAN COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [H.sapiens]
488642	0.6541915	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
1640821	0.920874	ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]

742707	0.8515067	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PRECURSOR [H.sapiens]
2029173	1.0094499	ESTs, Weakly similar to N-WASP [H.sapiens]
743589	0.8514377	ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]
35147	1.2581066	ESTs, Weakly similar to unnamed protein product [H.sapiens]
488202	0.932881	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTEIN ZAP128 [H.sapiens]
796542	-1.4697418	ets variant gene 5 (ets-related molecule)
811837	-1.157587	eukaryotic translation elongation factor 1 alpha 1
811837	-1.2030392	<b>eukaryotic translation elongation factor 1 alpha 1</b>
752631	0.6473517	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)
789012	0.8351735	fibulin 2
131839	-1.3048208	folate receptor 1 (adult)
52419	-1.2447753	Friedreich ataxia region gene X123
2309073	0.8484971	frizzled (Drosophila) homolog 5
298122	-1.3364021	frizzled (Drosophila) homolog 7
1393018	0.8376676	general transcription factor IIIC, polypeptide 1 (alpha subunit, 220kD )
741474	1.0870449	glucose phosphate isomerase
1609836	0.9886168	glutamate-ammonia ligase (glutamine synthase)
731044	0.8716644	glutaredoxin 2
344720	-1.6567437	glycophorin C (Gerbich blood group)
686552	0.9182272	golgi phosphoprotein 1
1556433	-1.0887923	GRO3 oncogene
796181	-1.2276581	growth arrest-specific 6
788654	0.7244749	<b>growth factor receptor-bound protein 2</b>
788654	1.2573483	growth factor receptor-bound protein 2
810063	0.6286184	growth factor, erv1 ( <i>S. cerevisiae</i> )-like (augmenter of liver regeneration)
308466	0.771216	GTP-binding protein Sara
283919	1.2112507	H2A histone family, member L
488964	1.3447179	H2A histone family, member O
290841	1.1670252	H2B histone family, member A
1500000	1.2926116	H2B histone family, member B
430235	0.7162503	H2B histone family, member Q
471568	1.1673113	hematological and neurological expressed 1

1569187	-1.4872982	heparan sulfate (glucosamine) 3-O-sulfotransferase 4
770845	0.7068283	hexokinase 1
345787	0.6981453	highly expressed in cancer, rich in leucine heptad repeats
172517	0.7779159	hippocalcin-like 1
323780	-1.0027215	Homo sapiens cDNA FLJ11177 fis, clone PLACE1007402
1474424	0.7689082	Homo sapiens cDNA FLJ12758 fis, clone NT2RP2001328
212542	0.7585053	Homo sapiens cDNA FLJ12900 fis, clone NT2RP2004321
270826	-0.9896888	Homo sapiens cDNA FLJ13329 fis, clone OVARC1001795
1492780	0.6923749	Homo sapiens cDNA FLJ14459 fis, clone HEMBB1002409
770675	0.6315109	Homo sapiens cDNA: FLJ21323 fis, clone COL02374
131094	0.7626373	Homo sapiens cDNA: FLJ21587 fis, clone COL06946
814528	0.7845635	Homo sapiens cDNA: FLJ22139 fis, clone HEP20959
753071	-1.2005994	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
840266	-1.200789	Homo sapiens cDNA: FLJ22667 fis, clone HSI08385
727078	0.7184618	Homo sapiens cDNA: FLJ23602 fis, clone LNG15735
796723	0.9915885	Homo sapiens clone CDABP0014 mRNA sequence
488404	-1.0484323	Homo sapiens clone TUA8 Cri-du-chat region mRNA
743977	0.6729967	Homo sapiens mRNA for TL132
327506	0.6943362	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 327506
44292	0.831599	Homo sapiens mRNA; cDNA DKFZp434C107 (from clone DKFZp434C107)
1871116	-1.209237	Homo sapiens mRNA; cDNA DKFZp434C1714 (from clone DKFZp434C1714); partial cds
2016648	0.917373	Homo sapiens mRNA; cDNA DKFZp434N1728 (from clone DKFZp434N1728)
565319	1.2155833	Homo sapiens mRNA; cDNA DKFZp564B1264 (from clone DKFZp564B1264)

813265	-1.3632094	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
486683	-1.1548164	Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323)
1461477	0.6300096	Homo sapiens mRNA; cDNA DKFZp586I0324 (from clone DKFZp586I0324)
1584540	-1.0933558	Homo sapiens mRNA; cDNA DKFZp586M2022 (from clone DKFZp586M2022)
132857	-1.280579	Homo sapiens mRNA; cDNA DKFZp586N1323 (from clone DKFZp586N1323)
22917	-1.2164705	Homo sapiens mRNA; cDNA DKFZp761M0111 (from clone DKFZp761M0111)
1631735	0.6404771	Homo sapiens, clone IMAGE:3604336, mRNA, partial cds
292770	0.6609782	Homo sapiens, clone IMAGE:3627860, mRNA, partial cds
810002	-1.3553375	Homo sapiens, clone MGC:19762 IMAGE:3636045, mRNA, complete cds
1492238	0.8804306	HSPC003 protein
796469	1.4207633	HSPC150 protein similar to ubiquitin-conjugating enzyme
470099	0.7443747	HT002 protein; hypertension-related calcium- regulated gene
178805	1.0513873	Human DNA sequence from clone RP5-850E9 on chromosome 20. Contains part of the gene for a novel C2H2 type zinc finger protein similar to <i>Drosophila Scratch</i> ( <i>Scrt</i> ), <i>Slug</i> and <i>Xenopus Snail</i> , a novel gene similar to <i>Drosophila CG6762</i> , STSs, GSSs and five CpG
811585	0.738212	huntingtin (Huntington disease)
1554549	1.2787033	hydroxyacyl glutathione hydrolase
813419	0.6951349	hydroxyacyl-Coenzyme A dehydrogenase, type II
256619	0.6797698	hydroxysteroid (17-beta) dehydrogenase 7
595213	0.8978322	hypothetical protein
785766	0.7476331	hypothetical protein
810402	0.6978141	hypothetical protein
811848	-1.2011809	hypothetical protein
489351	0.7422879	hypothetical protein DKFZp566J2046
66406	0.8888639	hypothetical protein DKFZp762E1312
292936	0.7154295	hypothetical protein FLJ10468

753299	0.9019921	hypothetical protein FLJ10504
504308	0.8199799	hypothetical protein FLJ10540
246800	0.6867481	hypothetical protein FLJ10803
343695	-1.002495	hypothetical protein FLJ10875
2052113	0.8477245	hypothetical protein FLJ10903
768570	0.732628	hypothetical protein FLJ11280
589232	0.6865999	hypothetical protein FLJ11506
489594	0.645574	hypothetical protein FLJ11565
41569	0.691145	hypothetical protein FLJ12650
785795	0.6683919	hypothetical protein FLJ12910
150003	0.8447372	hypothetical protein FLJ13187
1605426	0.8317254	hypothetical protein FLJ13352
248649	0.7210707	hypothetical protein FLJ13910
1554167	-1.3141843	hypothetical protein FLJ14529
1505038	1.3277637	hypothetical protein FLJ20171
502774	0.6807524	hypothetical protein FLJ20623
1636092	0.8841788	hypothetical protein FLJ20657
300632	-1.449587	hypothetical protein FLJ21044 similar to Rbig1
429799	0.8386406	hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2
510575	0.6295917	hypothetical protein FLJ22087
2015517	0.6441737	hypothetical protein FLJ22237
753378	0.7492212	hypothetical protein FLJ22649 similar to signal peptidase SPC22/23
144880	0.6902434	hypothetical protein from EUROIMAGE 1759349
1696757	0.6599512	hypothetical protein KIAA1165
824879	0.7333071	hypothetical protein MGC11275
325606	0.6225147	hypothetical protein MGC14353
1898619	0.6651268	hypothetical protein MGC15737
68636	0.6778817	hypothetical protein MGC2477
490023	-1.1020527	hypothetical protein MGC2648
1869201	0.8825788	hypothetical protein MGC2745
51773	0.8588635	hypothetical protein MGC3077
37708	0.7163849	hypothetical protein MGC3101
814443	-1.0250673	hypothetical protein MGC3232
120271	0.6562017	hypothetical protein MGC4692
812238	1.2664748	hypothetical protein MGC4692
1858892	0.9669022	hypothetical protein MGC4825
121251	0.6596925	hypothetical protein MGC5576
293727	0.6728542	hypothetical protein MGC861
745606	1.0663136	hypothetical protein PP591
2028949	0.8358024	hypothetical protein PRO1855
625399	-1.0594452	hypothetical protein similar to beta-transducin family

897806	0.7388301	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
39884	0.7526496	IMP (inosine monophosphate) dehydrogenase 1
221295	0.7342275	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
788234	-1.1061158	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
207288	0.7058528	insulin induced gene 1
130201	-1.2181641	intercellular adhesion molecule 2
782513	0.8030042	interferon, alpha-inducible protein (clone IFI-6-16)
84295	0.6876167	interleukin 1 receptor antagonist
811920	-1.5255258	interleukin 11 receptor, alpha
80344	-1.0602825	interleukin 7 receptor
869375	0.808792	isocitrate dehydrogenase 2 (NADP+), mitochondrial
868128	0.8970146	JM4 protein
824962	0.7238234	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
773922	0.7799164	KIAA0005 gene product
686172	0.846207	KIAA0008 gene product
814054	1.0130821	KIAA0040 gene product
898032	0.9547022	KIAA0097 gene product
530310	0.6682042	KIAA0143 protein
782428	1.0008279	KIAA0250 gene product
809944	0.7139515	KIAA0310 gene product
753162	-1.0119485	KIAA0603 gene product
124447	0.6363079	KIAA1184 protein
1518402	0.6378481	KIAA1361 protein
277571	-0.9977509	KIAA1706 protein
343731	0.6424907	<b>Kruppel-like factor 2 (lung) (KLF2), Homo sapiens</b>
280249	0.64759	Kruppel-like factor 7 (ubiquitous)
280907	-0.9932806	Kruppel-type zinc finger protein
770355	0.6829507	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)
767202	-1.4573536	latent transforming growth factor beta binding protein 2
199403	1.0142329	lectin, galactoside-binding, soluble, 8 (galectin 8)
2056139	-1.3506352	LIM domain protein
1469377	-1.359583	lipoma HMGIC fusion partner-like 2
150314	0.739762	lysophospholipase I
826363	0.6322533	lysophospholipase II

200814	-1.8295958	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)
729975	0.8385313	meningioma expressed antigen 5 (hyaluronidase)
1518890	0.6251884	metallothionein-like 5, testis-specific (tesmin)
2014034	0.9619198	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
124298	0.7507816	microsomal glutathione S-transferase 3
564492	0.7301895	mitochondrial carrier homolog 2
491524	0.6424448	mitochondrial ribosomal protein L13
2019223	0.7893602	mitochondrial ribosomal protein L17
782608	0.698569	mitochondrial ribosomal protein L9
590774	0.657447	mitogen-activated protein kinase 13
1473274	-1.3200174	myosin regulatory light chain 2, smooth muscle isoform
629944	0.6950339	myosin VB
841308	-1.3246996	myosin, light polypeptide kinase
1456348	0.7401571	N-acetylneuraminc acid phosphate synthase; sialic acid synthase
76605	0.7376829	nesca protein
838478	-1.2349342	neurocalcin delta
877621	-1.1422087	nGAP-like protein
199645	0.769591	nicastrin
811761	0.7578696	Nijmegen breakage syndrome 1 (nibrin)
75859	-1.5303427	N-myc downstream-regulated gene 2
845363	0.714201	non-metastatic cells 1, protein (NM23A) expressed in
203003	0.6802818	non-metastatic cells 4, protein expressed in
416959	-1.0566462	nuclear factor I/B
503851	0.6291771	nuclear receptor co-repressor/HDAC3 complex subunit
773188	0.6448143	nuclear receptor subfamily 1, group D, member 2
756442	0.7016064	P450 (cytochrome) oxidoreductase
1882697	-1.715818	peanut ( <i>Drosophila</i> )-like 2
416676	-1.0568729	pellino ( <i>Drosophila</i> ) homolog 1
285377	-1.4496786	pellino ( <i>Drosophila</i> ) homolog 2
1587710	-1.0209983	period ( <i>Drosophila</i> ) homolog 1
1573251	0.7816689	peroxisomal long-chain acyl-coA thioesterase
897963	-1.0075423	phosphatidic acid phosphatase type 2A
625923	0.8821749	phosphoenolpyruvate carboxykinase 2 (mitochondrial)

712401	-1.1218827	phosphoinositide-3-kinase, catalytic, delta polypeptide
272529	0.9423688	phosphomannomutase 2
843195	0.8606568	phosphoserine phosphatase
503215	0.8286483	pilin-like transcription factor
810124	0.8891272	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
290378	-0.9932643	podocalyxin-like
859761	0.6846134	poliovirus receptor-related 2 (herpesvirus entry mediator B)
744047	0.6748419	polo (Drosophila)-like kinase
897813	0.6741253	polyadenylate binding protein-interacting protein 1
813410	0.7093173	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)
67741	-1.3014364	PP2135 protein
241348	0.757138	prenylcysteine lyase
280375	0.9793036	PRO2000 protein
41698	0.6327738	progesterone binding protein
810558	0.943041	proteasome (prosome, macropain) 26S subunit, ATPase, 4
2050827	0.7211304	proteasome (prosome, macropain) 26S subunit, ATPase, 5
1553306	0.7471557	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
823598	1.1425746	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
2054635	1.0613961	proteasome (prosome, macropain) subunit, alpha type, 7
122241	0.939204	proteasome (prosome, macropain) subunit, beta type, 2
951233	0.8614727	proteasome (prosome, macropain) subunit, beta type, 3
1460110	0.7559869	proteasome (prosome, macropain) subunit, beta type, 5
2055807	0.638184	protein kinase domains containing protein similar to phosphoprotein C8FW
205049	0.6231646	protein kinase H11; small stress protein-like protein HSP22
41356	0.6961169	protein phosphatase 2, regulatory subunit B (B56), alpha isoform
358162	0.6999211	protein predicted by clone 23627
785707	0.8176557	protein regulator of cytokinesis 1
83363	0.7435058	protein-L-isoaspartate (D-aspartate) O-methyltransferase
303109	-1.0807576	purinergic receptor (family A group 5)

1917941	1.1872008	purine-rich element binding protein B
685516	0.7378926	putative G protein-coupled receptor
122077	1.2576139	putative membrane protein
365060	0.6350631	RAB11A, member RAS oncogene family
79520	0.9457391	RAB2, member RAS oncogene family
1911343	0.9110591	RAB26, member RAS oncogene family
1639531	0.7033264	RAB27A, member RAS oncogene family
1845169	0.8131362	RAB35, member RAS oncogene family
470124	0.8347241	RAD1 ( <i>S. pombe</i> ) homolog
1476053	0.7367106	RAD51 ( <i>S. cerevisiae</i> ) homolog ( <i>E. coli</i> RecA homolog)
505864	-1.0033263	RalGDS-like gene
45099	-1.566311	regucalcin (senescence marker protein-30)
2106144	-1.1719133	regulated in glioma
813707	0.6814476	regulator of G-protein signalling 16
781097	0.9100493	reticulon 3
2322367	0.9859632	reticulon 4
595037	1.2486446	retinoic acid induced 3
812994	0.6420817	retinoid X receptor, alpha
244801	0.908481	Rho guanine exchange factor (GEF) 11
1422338	0.7690604	ribonucleotide reductase M2 polypeptide
869450	-0.9934083	ribosomal protein L11
990881	-1.0640807	<b>ribosomal protein L12 (Rpl12), mus musculus</b>
307029	-1.0497874	ribosomal protein L26
322561	-1.1270333	ribosomal protein L31
469686	0.9381847	Ric ( <i>Drosophila</i> )-like, expressed in many tissues
291478	-1.0400846	runt-related transcription factor 3
810612	0.7419597	S100 calcium-binding protein A11 (calgizzarin)
785840	0.6800437	SEC24 ( <i>S. cerevisiae</i> ) related gene family, member D
2306987	0.6501071	secreted and transmembrane 1
878836	-1.2200837	secretory granule, neuroendocrine protein 1 (7B2 protein)
1492463	0.8360771	selenoprotein X, 1
814378	0.8015236	serine protease inhibitor, Kunitz type, 2
209066	0.8582298	serine/threonine kinase 15
209066	1.0066096	<b>serine/threonine kinase 15</b>
161456	-1.0220494	serum amyloid A1
1917449	-1.217371	serum amyloid A4, constitutive
470061	0.9920108	seven in absentia ( <i>Drosophila</i> ) homolog 2
49351	0.6551453	SEX gene
343760	-1.0803279	SH3 domain binding glutamic acid-rich protein like 2

2302099	0.6386686	sialidase 3 (membrane sialidase)
813751	0.7665427	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)
785616	0.6800658	signal sequence receptor, alpha (translocon-associated protein alpha)
2504881	-1.1674204	signal transducer and activator of transcription 5A
140574	-1.103064	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin)
704414	0.8498631	small nuclear ribonucleoprotein polypeptides B and B1
288999	0.8593924	small protein effector 1 of Cdc42
810762	0.6371461	SNARE protein
49273	0.635859	solute carrier family 27 (fatty acid transporter), member 4
823871	-1.2090693	SPARC-like 1 (mast9, hevin)
1734309	0.666164	sperm associated antigen 4
124781	0.6809199	squalene epoxidase
1558675	-1.2313679	SRY (sex determining region Y)-box 10
1469425	0.8391993	SRY (sex determining region Y)-box 22
1476065	0.6783519	stathmin 1/oncoprotein 18
810711	1.1074523	stearoyl-CoA desaturase (delta-9-desaturase)
590759	0.672734	sterol-C4-methyl oxidase-like
366132	1.1440486	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD
781014	-1.2659158	suppression of tumorigenicity 5
969877	0.6564571	synaptosomal-associated protein, 25kD
509588	0.6903363	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD
1474955	0.8573467	TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA-binding protein 56)
47043	-1.0841886	tensin
789376	0.6883473	thioredoxin reductase 1
825470	0.9274271	topoisomerase (DNA) II alpha (170kD)
1591264	0.6337293	transaldolase 1
347373	1.0454939	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)
705064	0.8401441	transforming, acidic coiled-coil containing protein 3
359887	1.1837896	translocase of inner mitochondrial membrane 17 (yeast) homolog A

149355	0.8134342	translocating chain-associating membrane protein
826256	0.7092586	transmembrane 7 superfamily member 1 (upregulated in kidney)
740620	-1.071175	tropomyosin 2 (beta)
611532	-1.3689616	troponin I, skeletal, fast
1409509	0.8339967	troponin T1, skeletal, slow
825585	0.741258	tubulin-specific chaperone e
814306	0.6963874	tumor protein D52
1435003	0.8311727	tumor suppressing subtransferable candidate 1
769921	0.9944462	ubiquitin carrier protein E2-C
839682	0.8696528	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)
289978	0.7931469	ubiquitin-like 4
824524	0.6424419	UDP-galactose transporter related
236034	0.673506	uncoupling protein 2 (mitochondrial, proton carrier)
1631699	0.7115561	valosin-containing protein
810316	0.6323393	very long-chain acyl-CoA synthetase; lipidosin
731023	0.7032815	WD repeat domain 5
268946	0.6881593	WD40 protein Ciao1
138189	0.7953361	Wolfram syndrome 1 (wolframin)
813281	0.8016742	WW domain-containing protein 1
813629	0.7102574	YME1 ( <i>S.cerevisiae</i> )-like 1

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